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OM nucleic - nucleic search, using sw model

Run on: August 21, 2001, 18:21:27 ; Search time 94.78 Seconds

(without alignments)  
6924.896 Million cell updates/sec

Title: US-09-719-272-1

Perfect score: 3467

Sequence: 1 gatcgcagctgaagatcc.....attgataatcagattctt 3467

Scoring table: IDENTITY\_NUC  
Gap 10.0, Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: Issued\_Patents\_NA:\*  
2: /cgn2\_6/prodata/1/lna/5A.COMB.seq:\*  
3: /cgn2\_6/prodata/1/lna/5B.COMB.seq:\*  
4: /cgn2\_6/prodata/1/lna/6A.COMB.seq:\*  
5: /cgn2\_6/prodata/1/lna/6B.COMB.seq:\*  
6: /cgn2\_6/prodata/1/lna/PCITUS.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1285	37.1	6000	US-08-348-006B-6	Sequence 6, Appl
2	1285	37.1	6000	US-08-800-825A-6	Sequence 6, Appl
3	1285	37.1	6000	US-09-158-657-6	Sequence 6, Appl
4	1285	37.1	6000	PCT-US94-10166-6	Sequence 6, Appl
5	1273.2	36.7	5690	US-08-447-464-2	Sequence 2, Appl
6	1273.2	36.7	5690	US-08-716-679-2	Sequence 2, Appl
7	552	15.9	2872	US-08-015-985-2	Sequence 4, Appl
8	537.4	15.5	2409	US-08-015-985-2	Sequence 4, Appl
9	361.8	10.4	5769	US-08-652-971-1	Sequence 1, Appl
10	361.8	10.4	5769	US-08-991-953A-1	Sequence 1, Appl
11	361.8	10.4	5769	US-08-449-644-3	Sequence 3, Appl
12	361.8	10.4	5769	US-08-449-644-3	Sequence 3, Appl
13	335.6	9.7	4374	US-08-449-644-3	Sequence 3, Appl
14	335.6	9.7	4374	US-08-449-644-3	Sequence 3, Appl
15	308	8.9	4651	US-08-015-973-2	Sequence 4, Appl
16	308	8.9	4651	US-08-015-973-2	Sequence 4, Appl
17	260.2	7.5	6924	US-08-448-164-2	Sequence 2, Appl
18	260.2	7.5	6924	US-08-448-164-2	Sequence 2, Appl
19	245	7.1	4338	US-08-015-986A-1	Sequence 1, Appl
20	245	7.1	4338	US-08-015-986A-1	Sequence 1, Appl
21	194.4	5.6	3869	US-08-241-853-1	Sequence 1, Appl
22	194.4	5.6	3869	US-08-241-853-1	Sequence 1, Appl
23	189.2	5.5	5117	US-08-854-585-1	Sequence 1, Appl
24	189.2	5.5	5117	US-08-854-585-1	Sequence 1, Appl
25	178.6	5.2	2943	PCT-US95-05512-1	Sequence 1, Appl
26	178.6	5.2	2943	US-08-548-159-2	Sequence 4, Appl
27	176.8	5.1	5455	US-08-342-930-1	Sequence 1, Appl

28	168.4	4.9	1413	2	US-08-239-276-9	Sequence 9, Appl
29	168.4	4.9	1413	2	US-08-468-579B-9	Sequence 9, Appl
30	168.4	4.9	1413	2	US-08-468-579B-9	Sequence 9, Appl
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33	168.4	4.9	3311	3	US-08-468-579B-10	Sequence 10, Appl
34	161.2	4.6	4799	1	US-08-201-697-6	Sequence 6, Appl
35	160.6	4.6	4799	1	US-08-201-697-6	Sequence 6, Appl
36	160.6	4.6	4815	1	US-08-201-697-3	Sequence 3, Appl
37	160.6	4.6	5679	1	US-08-201-697-3	Sequence 3, Appl
38	158.4	4.6	2309	1	US-08-036-210-10	Sequence 10, Appl
39	158.4	4.6	2309	2	US-08-449-609-14	Sequence 14, Appl
40	158.4	4.6	2692	2	US-08-036-210-14	Sequence 14, Appl
41	158.4	4.6	2692	2	US-08-449-609-14	Sequence 14, Appl
42	158.4	4.6	3973	1	US-08-036-210-21	Sequence 21, Appl
43	158.4	4.6	3973	2	US-08-449-609-21	Sequence 21, Appl
44	151.4	4.4	2145	1	US-08-202-389-5	Sequence 5, Appl
45	151.4	4.4	2277	3	US-09-358-685-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-348-006B-6  
Sequence 6, Application US/08348006B  
Patent No. 5658756  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHMIDT, AZRIEL  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN.  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. MARK HAND  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,006B  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,032  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J., MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 189921A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6000 base pairs  
TYPE: nucleic acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-348-006B-6

Query Match 37.18; Score 1285; DB 1; Length 6000;  
Best Local Similarity 81.48; Pred. No. 0;  
Matches 1489; Conservative 0; Mismatches 340; Indels 0; Gaps 0;

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OY 89 ccaaccacccatccccatccatccacgacccctgagcaaacatcgagccctcaaaagcaaga 148
DB 4018 CCACCCCCCAATTCCTCCATCCAGACATGCGGAGCAGACGAGGCGGCTCAAGGCCAAGCA 4077
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DB 4078 CACCTTCACAGCTCTCCACGAGATGAGTCATCAACCTTGACAGCGATTACATGGA 4137
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DB 4138 AACTTCACACCTTGGAAGTGAACACCCGAAACCGGCTATGCCAACGCTACCTGCTATGA 4197
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DB 5098 TGTGAGAGCCTTGATCTACATCAACGCGCATTTATGATGAGTACAGGACGAGAAAGGC 5157
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DB 5158 CTACTAGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5217
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DB 5758 AAGCCATGCTCCCGCCAGCGCCGACACC 5786

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RESULT
2
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: Sequence 6, Application US/08800825A
: Patent No. 5866397
: GENERAL INFORMATION:
: APPLICANT: RODAN, GIDEON A.
: APPLICANT: SCHMIDT, AZRIEL
: APPLICANT: RUTLEDGE, SU JANE
: TITLE OF INVENTION: CODA ENCODING A NOVEL HUMAN PROTEIN
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
: STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
: CITY: RAHWAY
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07065-0900
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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1 COMPUTER: IBM PC compatible  
 2 OPERATING SYSTEM: PC-DOS/MS-DOS  
 3 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 4 CURRENT APPLICATION DATA:  
 5 APPLICATION NUMBER: US/08/800,825A  
 6 FILING DATE: 14-FEB-1997  
 7 CLASSIFICATION: 435  
 8 ATTORNEY/AGENT INFORMATION:  
 9 NAME: HAND, J. MARK  
 10 REGISTRATION NUMBER: 36,545  
 11 REFERENCE/DOCKET NUMBER: 189922DA  
 12 TELECOMMUNICATION INFORMATION:  
 13 TELEPHONE: 732-594-3905  
 14 TELEFAX: 732-594-4720  
 15 INFORMATION FOR SEQ. ID NO.: 6:  
 16 SEQUENCE CHARACTERISTICS: **Y**  
 17 LENGTH: 6000 base pairs  
 18 TYPE: nucleic acid  
 19 STRANDEDNESS: single  
 20 TOPOLOGY: linear  
 21 MOLECULE TYPE: CDNA  
 22 US-08-800-825A-6

Query Match	37.1%	Score 1285;	DB 2;	Length 6000;
Best Local Similarity	81.4%;	Pred. No. 0;		
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Oy	89	ccaccaccacatcccacatccagacacttggcgcagacatcgacgcctcaagaagcaaga	148	
Db	4018	CCACCCGCAATTCCTCATGCGACATATGGCGGACACACGACGCCCTCAAGCCCAAGCA	4077	
Oy	149	tggcctcaagttctccagggatgttggtccatccagaccttgacagcaattcacgttgcga	208	
Db	4078	CAGCCTCAAGGCTCCCGAGGATATGATCTCATCGACCTTGACAGCACTTCATATGGGA	4137	
Oy	209	gaattcaaaccttggaagtgtgaacagcccaagaacgcgtatgtgaatgtcatcgtccatga	268	
Db	4138	ACATTTCAACTGTGAAGTGAACAGCGGAAGCAACCCGTAATGCCAACGTCATTCGCTTAGA	4197	
Oy	269	ccacctctcgatcatccttaccctctatcgatgtgcgtcccgaggatgtacatcaatctgc	328	
Db	4198	CCACTTCCCGTGTATCTCCACGCCATTTAAGGCATATAGGCACTGATGATTCATCAATATGC	4257	
Oy	329	caactatcatcgatggttacgcagacagaaatgctctacatgcacgcagagggcccttcgc	388	
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Oy	389	ccggaccatcggcgatctcttgagaaatgtgtgtggaacagagcgccacctgtgtcat	448	
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D	b	4678	CAGTCGGCGGTGGGCCCCACAGCCTCCTTATCTGTCTACGACGCCATCTTGAGCGGAT	4737
O	y	809	gaagacgaagaaagcgtgtgacatctatgtgcacgtgtacgtcatgcatgcatcagaaagaa	868
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D	b	4858	GGCTGTGGCAACACAGAAAGTGGCCCGACGAGCCTCTATGCTCAATCCAGAAAGCTGAC	4917
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D	b	4918	CCAGGTGAGACCTGGCGGAACAGTACTCGCATGGAACTGGAGTTCAAGCGCTGGCTAA	4977
O	y	1049	ctccaaagcccaacgctcccgcttcatagcgccaacctgccttgcaaacagttaagaa	1108
D	b	4978	CTCCAAAGGCCCAACAGTCAAGCTTCATGAGTCCATCTGCTTGAATAAGTTCAAGAA	5037
O	y	1109	ccgagctgtgtgaacatcatatgccttaccgaattgaaaccggtgtgtctgcaagcagaagc	1168
D	b	5038	CCGCTGTGTGAACATCATATGCCCCCTATGAGAGCACACGGGCTGTGCTGCAACCATCCGGG	5097
O	y	1169	tgtgtgagagctctgtacatcatcaatgtccagcttccggtgtgtatagaacagaagaagc	1228
D	b	5098	TGTGAGAGGCTCTGTGACATCATCAACGCCACACTTATTAAGTGCCTCAAGCAGCAAGAGGC	5157
O	y	1229	ctacatagctacacaagggggcctctgtgcagaaagaaaccggaagctctgtgcagatgtatg	1288
D	b	5158	CTACATCCCGACACAGAGGGCCGCTGGCGGAGACCAACGGAAGACTTGTGGCATTGCTGTG	5217
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D	b	5218	GGAGAACAATTTCGACATCTGTGTGTGTGACCAAGCTTGGGGAATGGCGCGGAGAA	5277
O	y	1349	atgcaccagctactgggcagcagaagcgctctgtctgtctaccagaactgtgtgtaaccc	1408
D	b	5278	GTCACACACTACTGCGCGGCGGACCGCTGCGCGCTACCAAGTCTTGTTGTTAATCC	5337
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D	b	5338	GATGCGCAGATTAATACATCTCTCACTATATCTCGAAGGTTCAAGATCAAGATGCCG	5397
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D	b	5638	TCAACAGCTGAAGATGCTACGAACCCAGGGCGCGCCATGTGTGCACAGACAGGATAGTA	5697
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Db 5698 CCAAGTTCCTGTTACAGGGGCACTGAGTACCTCGAAGCTTTGACACTATGCAACCTA 5757  
QY 1829 actacgctccctcctcctcctcgcacccc 1857  
Db 5758 AAGCCATGTCCTCCCGCCAGCCGACAC 5786

## RESULT 3

US-09-158-657-6  
Sequence 6, Application US/09158657  
Patent No. 6214564  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANEY  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/158,657  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/800,825  
FILING DATE: 14-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J. MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18992DA  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6000 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-158-657-6

Query Match 37.18; Score 1285; DB 4; Length 6000;  
Best Local Similarity 81.48; Pred. No. 0;  
Matches 1489; Conservative 0; Mismatches 340; Indels 0; Gaps 0;

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QY 89 ccaaccacacatcccaatccacagacgtcgagagacatcgagcgctcacaagcaaga 148  
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QY 569 cactgtgcacctcgcacatcccaagagtgctcagtgagagagcgtgagctgtca 628  
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QY 629 gtccatctcagcctgagcagacatgagtgatcctgagtaaccaactccatcctgac 688  
Db 4558 GTTCACAGTTACGCGCTGCGGCGGACCATGGCTGCGGAAATCCCAACGCCCTTCTG 6617  
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QY 809 gaagcagagagagagcgtgagacatctatgacacagcagcagcagcagcagcagcag 868  
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PCT-US94-10166-6

sequence b, Application PC/TUS9410166  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOHN W. WALLEN III  
STREET: P. O. BOX 2000, 126 E. LINCOLN AVE.  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10166  
FILING DATE: 09-SEPT-1994  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,032  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WALLEN, JOHN W III  
REGISTRATION NUMBER: 35403  
REFERENCE/DOCKET NUMBER: 18992  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720

PCT-US94-10166-E

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Query Match      37.1%; Score 1285; DB 5; Length 6000;
Best Local Similarity 81.4%;
Matches 1489; Conservative 0;

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QY	29		

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4198 CCACTCCGTCATCTCCAGCCCATGAAAGCATATCCCACTA

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4318 ~~cccccc~~ccgagaaatgctgctggaaacagcgcaagcgccactgtgtcat 448  
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449 qatgacacacctcttgcggcaccatcgta 4377

4378 GATGACGGCGCTTGAGCACACTCCTAAGCCCGTGG 508

509 caccgagacctgtgacctatcgaatnaccctat  
-----cccccaaaagg 4437

4438 CACGAGACTACGGCTTCATCCAGGTCAAGTTGCTAGATACCCTCCTT

500 caccgtgcaccttcgcactccacaagagtgtgctccagtqaqaaacatatgaactcccttcc

530  
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4558 CTTCTGAGTCTCTGAGTACCAACTCCATCTGCG 688

689 cttcctacgaccgtatcttcccttcctggc 4617

4618 TTTCCGCGAGACTCAGACCTTCATGGCACTG 748

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.....GCGATGGCCACGTGACGCTCATGAGTCCACGCCAA 4797



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Db      5039  CCCAAGTCAGCGGGAAGGCTTACTTACTTACTTCATCGGCCCAATGCTCAATGAAGACCAAGACGAC  5098
Oy      1590  tttagaagaatgaggactatactcagtgactcagtgctgagcgttgaggccgacacggagt  1649
Db      5099  TTTGGCCAGGATGGGCCCATCTCGGTGCACAGTAGTGTGCAATGGCGACCGGAGTA  5158
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Oy      1888  ctctgagc 1895
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RESULT 6
US-08-716-679-2
: Sequence 2, Application US/08716679
: Patent No. 5846800
: GENERAL INFORMATION:
: APPLICANT: Schlessinger, Joseph
: APPLICANT: Yan, Hai
: TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
: TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/716,679
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/130,570
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Mistrock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 7683-043
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-790-9090
: TELEFAX: 212-869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5690 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: unknown

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TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 833..5338  
 US-08-716-679-2

Query Match 36.7% Score 1273.2; DB 2; Length 5690;  
 Best Local Similarity 80.5% Pred. No. 2,6e-299;  
 Matches 1503; Conservative 0; Mismatches 363; Indels 2; Gaps 1;

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OY 1770 cagctgagagagagagagagagagagagagagagagagagagagagagagagagagag 1829
DB 5279 CAGTTCGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1830
OY 1830 -ctaacgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1887
DB 5339 GCCATGAGGCGCGCCAGACACCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1888
OY 1888 ctctgagag 1895
DB 5399 CTGCGTGC 5406

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RESULT 7  
 US-08-015-985-4  
 ; Sequence 4, Application US/08015985  
 ; Patent No. 553886  
 ; GENERAL INFORMATION:

APPLICANT: Schlessinger, Joseph  
 APPLICANT: Sap, Jan M.  
 TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTRANSFERASE  
 TITLE OF INVENTION: PHOSPHATASE-ALPHA  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESSES: 14  
 ADDRESS: PENNIE & EDMONDS  
 STREET: 1155 AVENUE OF THE AMERICAS  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/015,985  
 FILING DATE: 10-FEB-1993  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7683-020  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2872 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: unknown  
 MOLECULE TYPE: cDNA  
 US-08-015-985-4

Query Match 15.98: Score 552: DB 1: Length 2872:  
 Best Local Similarity 59.58: Pred. No. 1.8e-124:  
 Matches 977: Conservative 0: Mismatches 650: Indels 15: Gaps 2:

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 Oy 1083 aacctgc 1950  
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 Oy 1443 cgtgagtgatagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2427  
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Db	953	AMAAACGGGGAATGATTTCTTGGCCGAATGATCTGGAAACAAACACAGCACCATGTCTA	1011
Qy	448	tgtgtgcaagcgtctggaggaagaagtcctccgggtaaaatgtgtatgctatctgccaagccg	507
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Db	1073	GCTGTGACCTTAATGGGAAATTTGGGTCTCTTAAGATGTGACTGTCTGTGGTGAAT	1132
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Qy	622	-----tgctcagtttcagttcatgtgacctgtgccaagcatgaggtcttcgaataccaa	675
Db	1193	GCCTCATCTACTCAGTTTCCACTTACCAGCTGGCCAGACTTTGGGTGCTTTTACCCGA	1252
Qy	676	ctccacatccctgccttccctcgaagaggttcaaggtctgaacccccctagaagcaggccca	735
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Db	1313	TGCTGTCTCACCATGCAAGTGCAGGTGTAAGGGCTGTACAGGACTTTGTGCTATTAATGAGCA	1372
Qy	796	tgttggacggaatgaagcagaaagaggtgtgacatcttctgtgcaagctgacatgac	855
Db	1373	TGCTGACATGTATGTCATACAGAACGGAAGGTGACCTGTATGGCTTTGTGACCCGGATTC	1432
Qy	856	gatacagaaggaactaactgtgtgaagcaggaagcaagtaactgtgtatcctatcctatggagc	915
Db	1433	GGGCACACGGCTGCCAGATGGTGTGAAACCCATATGCAAGTATGCTTCATATACAAAGCC	1492
Qy	916	tgtgtgaagctgcacgltgcgcgcacacagaagtgtccgtccgcaactgtatgccca	975
Db	1493	TTCGTGGACATTATCTATGAGAGATACAGAACTGGAAGTGCCTCTGTAAACCCACCC	1552
Qy	976	tccgaagctgtggcgaagtgcctcccgagggggaagtgtgaacgcgaatggagctgaatca	1035
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Db	1673	ACATGAGAAGAACCGTGTATTACAGATCATTCATATGAATTAACAGAGTATCATATC	1732
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Db	1793	GGCAATAGAGACTCTTATATCCAGCCAGCAGGGCTTCTTCCACACAAATGAGGACTTCT	1852
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MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/991,258A  
 FILING DATE: 17-DEC-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/652,971  
 FILING DATE: 24-MAY-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-63478-3/WMD/MTK  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5769 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 379..4686  
 US-08-991-258A-1

Query Match	Best Local Similarity	Score	DB	Length
Query Match	Best Local Similarity	Score	DB	Length
Matches 935; Conservative	54.0%; Pred. No. 3,76-78;	361.8;	DB: 2	5769;
	1; Mismatches 758; Indels 39; Gaps			
Qy	89	ccaccaccaccatcccatccaccagacccctgagcgaacacatcgagcgccctcaagaacaga	148	
Db	2958	ccaccctgcagccgacagcagcctgctacaccttctcaacacatcattcaacagatgaagcacc	3017	
Qy	149	tggccctcaagttctcccaaggatgatgatgatgatgatgatgatgatgatgatgatgatgat	208	
Db	3018	ggcctcagcagccttcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	3017	
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US-08-769-399-1
? Sequence 1, Application US/08769399
? Patent No. 5976852
? GENERAL INFORMATION:
? APPLICANT: Cheng, J111
? APPLICANT: Lasky, Laurence A.
? TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
? NUMBER OF INVENTION: PHOSPHATASE, PTP LAMBDA
? NUMBER OF SEQUENCES: 10
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 460 Point San Bruno Blvd.
? CITY: South San Francisco
? STATE: California
? COUNTRY: United States
? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/769.399
? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Dreger, Ginger R.
? REGISTRATION NUMBER: 33,055
? REFERENCE/DOCKET NUMBER: P1033
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 225-3216
? TELEFAX: (415) 952-9881
? TELEX: 910 371-7168
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5769 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 379..4686
? US-08-769-399-1

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	Query Match	Best Local Similarity	10.48	Score 361.8	DB 2	Length 5769
	Matches 935	Conservative	1	Mismatches 758	Indels	Gaps
Qy	89	ccaccaccaccatcccatcccatccagaccctgsgagcaacatgagcgccttaaaagcaacga				
Db	2958	ccaccctctgcacatcccgagtgctgacaccttcttccacacacatcattaaccttgaacacgacga				
Qy	149	tgagctcaagtctctccagaggaataagaatccatgagaccttgagcaagcaggttcacgttggga				
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Qy	269	ccacatctagagtcacatcccttaccctctatcgatgtggctcccgaggatgacacactcaatgc				
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RESULT 12  
 US-08-991-953A-1  
 : Sequence 1, Application US/08991953A  
 : Patent No. 6083748  
 : GENERAL INFORMATION:  
 : APPLICANT: Cheng, Jili  
 : APPLICANT: Laskey, Laurence A.  
 : TITLE OF INVENTION: A NOVEL KAPPA/MU-LINE PROTEIN TYROSINE  
 : TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
 : NUMBER OF SEQUENCES: 10  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP  
 : STREET: 4 Embarcadero Center, Suite 3400  
 : CITY: San Francisco  
 : STATE: California  
 : COUNTRY: United States  
 : ZIP: 94111  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/991,953A  
 : FILING DATE: 16-DEC-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/652,971  
 : FILING DATE: 24-MAY-1996  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Dreger, Walter H.  
 : REGISTRATION NUMBER: 24,190  
 : REFERENCE/DOCKET NUMBER: A-63478-3/RMD/MTK  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 781-1989  
 : TELEFAX: (415) 398-3249  
 : TELEX:  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 5769 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: DNA (genomic)

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by	89					

[illegible]

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RESULT 13
US-08-449-644-3
; Sequence 3, Application US/08449644
; Patent No. 5856162
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ullrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

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21P: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,644
FILING DATE: 24-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,244
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SPO ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 4374 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4371
US-08-449-644-3

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Query Match          9.7%  Score 335.6; DB 2; Length 4374;
Best Local Similarity 53.0%  Pred. No. 7.4e-72;
Matches 928; Conservative 0; Mismatches 774; Indels 48; Gaps 8;

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QY 270 caccctgagatccttaccctatcgaatggcgtcccgaggagtgactacaatgac 329
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RESULT 5  
 US-08-449-644-4  
 Sequence 4, Application US/08449644  
 Patent No. 5856162  
 GENERAL INFORMATION:  
 APPLICANT: Schlosssinger, Joseph  
 APPLICANT: Sep, Jan M.  
 APPLICANT: Ulrich, Axel  
 APPLICANT: Vogel, Wolfgang  
 APPLICANT: Fuchs, Miriam  
 TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHORYROSINE  
 TITLE OF INVENTION: PHOSPHATASE-KAPPA  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & EDMONDS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/449,644  
 FILING DATE: 24-MAY-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/087,244

[illegible]



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Job time: 7483 sec

Wed Aug 22 12:58:51 2001

us-09-719-272-1.rni

Page 20

Run on: August 21, 2001, 18:23:17 : Search time 309.69 seconds

10382.177 Million cell updates/sec

Title:	US-09-719-272-1
Perfect score:	3463

Sequence: 1 gatccgaactgaagaatctcc

Scoring table: IDENTITY\_NUC

Searched: 730101 seqs, 313950809 residues

number of hits satisfying chosen parameters: 1460202

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3467	100.0	3467	21	AAZ291907	Human protein tyrosine
2	3467	100.0	3467	21	AAZ59132	LAR tyrosine phosphatase
3	3463	99.9	7702	21	AAA88739	Human protein tyrosine
4	3463	99.9	7702	21	AAZ291908	Human protein tyrosine
5	3463	99.9	7702	21	AAZ59133	Human protein tyrosine
6	2934.4	84.1	3064	21	AAAF1575	LAR tyrosine phosphatase
7	1285	37.1	6000	16	AAO86478	Human prostate cancer
8	1285	37.1	6000	18	AAAT85389	Human PTP-OB. Hom
9	1285	37.1	6000	20	AAAO6095	Human protein tyrosine
10	1273.2	35.7	5690	16	AAO86902	Rat receptor type-1
11	1059	30.5	4555	16	AAO94311	Tyrosine phosphatase

12	970	28.0	1029	20	AAX24802
13	578.4	15.7	601	21	AAO243322
14	552	15.9	2872	17	AAQ21001
15	552	15.9	2872	17	AAT36881
16	532	15.9	2872	17	AAX29853
17	537.4	15.5	2409	17	AAT36882
18	537.4	15.5	2409	17	AAX29852
19	387.2	11.2	5581	19	AAV17098
20	361.8	10.4	5769	19	AAV15004
21	343	9.9	459	15	AAO58004
22	329.2	9.5	4374	15	AAO72914
23	317	9.1	421	15	AAO68703
24	308	8.9	4531	15	AAO72913
25	306.4	8.8	5775	20	AAZ08539
26	260.2	7.5	6924	15	AAO67283
27	245	7.1	4338	15	AAO71842
28	194.4	5.6	3969	19	AAV05762
29	194.4	5.6	3969	20	AAV81697
30	190.2	5.5	6075	21	AAAB8865
31	189.2	5.5	5117	16	AAO6027
32	184.4	5.3	188	21	AAAT0046
33	180.2	5.2	1163	18	AAAT95229
34	180.2	5.2	2464	18	AAAT95221
35	178.6	5.2	1110	18	AAAT67297
36	178.6	5.2	2840	18	AAAT67295
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38	178.6	5.2	2994	18	AAAT8479
39	178.6	5.2	3310	18	AAAT67296
40	178.4	5.1	1839	21	AAAB8865
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42	176.8	5.1	5455	19	AAVJ3577
43	173.2	5.0	2711	18	AAAT95222
44	172.2	5.0	2716	18	AAAT95231
45	172.2	5.0	3267	18	AAAT95220

## ALIGNMENTS

RESULT 1  
ID AA291907 standard; DNA; 3467 BP.  
XX  
AC AA291907;  
XX  
DT 07-JUN-2000 (first entry)  
XX  
DE Human protein tyrosine phosphatase specific antibody coding sequence.  
XX  
KW Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR;  
KW CD45; PTP; diabetes; insulin resistance related disease; syndrome X;  
KW non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;  
KW heart disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200002922-A1.  
XX  
PD 20-JAN-2000.  
XX  
PF 06-JUL-1999; 99WO-JP03656.  
XX  
PR 10-JUL-1998; 98WO-JP03120.  
XX  
PA (FUSO ) FUSO PHARM IND LTD.  
XX  
PI Yamamoto H, Tsujikawa K, Uchino Y;  
XX  
DR WPI; 2000-182215/16.  
XX  
DR P-PSDB; AAY81783.  
XX  
PT Antibody for diagnosis and treatment of insulin resistance disorders  
PT and syndrome X recognises the intracellular domains of tyrosine

PT phosphatase -  
 XX  
 PS Claim 6: Page 53-59; 83pp: Japanese.  
 XX

CC This sequence encodes an antibody of the invention that has sites  
 CC specifically recognizing the intracellular domains of the phosphatase  
 CC subunits LAR and Cdk5. The antibody recognises the intracellular domain  
 CC of two or more protein tyrosine phosphatases (PTPs). The antibody is  
 CC useful for the detection and assay of PTP including novel phosphatases  
 CC generated by cloning; and diagnosis, treatment and prevention of insulin  
 CC resistance related diseases and non-insulin dependent diabetes mellitus,  
 CC syndrome X and arteriosclerosis and heart disorders.  
 XX

Sequence 3467 BP: 783 A; 957 C; 957 G; 770 T; 0 other;

Query Match 100.0%; Score 3467; DB 21; Length 3467;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Oy 61 tcaactaccagagaccagagctgctgagagaccacccacccacccacccacccacccaccc 120  
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Db 781 tctgtatgtatgacatgttggagcagatgagcagagagacggtgagatctatgacc 840  
 Oy 841 acgtgagcctgagatgagatcaagagaaactatagttgacagcagagagacagatgct 900  
 Db 841 acgtgagcctgagatgagatcaagagaaactatagttgacagcagagagacagatgct 900  
 Oy 901 tcatcatagagcgtctgagagcgtgagcagctgagcagacacacacacacacacacacac 960  
 Db 901 tcatcatagagcgtctgagagcgtgagcagctgagcagacacacacacacacacacacac 960  
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 Oy 1021 tggagcctgagatccaagtctgagcagacacacacacacacacacacacacacacac 1080  
 Db 1021 tggagcctgagatccaagtctgagcagacacacacacacacacacacacacacacac 1080  
 Oy 1081 ccaacactgctctgacaagaatccaagaacgagctggtgaaatcatatgacctacgaattga 1140  
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 Oy 1141 cccgtgtgtctgacagcccatccgtgtgtgaggggtctgactatcaatgacagct 1200  
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 Db 1741 ctgcaatggttgagacagagacagatcagcctgtgctacacgtagcagccttggatgac 1800  
 Oy 1801 tcggagccttggacacacatgcaacgtaactacacgctcctcctcctcgcacaccccg 1860  
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 Oy 1861 cgtggggtcggaggggagac 1920

Dh	1861	cgtagggggtccgggggggagaccagctctctcttgagccataccgacscatgctccagccccc	1920
Oy	1921	tacgcagatgctgtctacgttcgacagacagccccacgggggataccagcgttttaaggaaagt	1980
Dh	1921	tacgcagatgctgtctacttgcgtcagagccacgggggataccagcgttttaaggaaagt	1980
Oy	1981	tgcacacccaataccagagagctctagaaacatccctctggtcgaagtgtgaatggtccagcggcagg	2040
Dh	1981	tgcacacccaataccagagagctctagaaacatccctctggtcgaagtgtgaatggtccagcggcagg	2040
Oy	2041	cactgtgagccctctctccacccagacccacccctgggggcccgcgtctcaagctctgttcgcg	2100
Dh	2041	cactgtgagccctctctccacccagacccacccctgggggcccgcgtctcaagctctgttcgcg	2100
Oy	2101	tccgcgaattctctcatgctctctctctgtaggtgtggtcttggtggcagaagctccctttaat	2160
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Dh	2161	acattaaagtgggttagacacgaaggagttttaaccctctccctctgaattctcttcgcga	2220
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Dh	2221	atccgatactctgcaagaaatgggccaactgttaaggtctggtttatgtttgttttttt	2280
Oy	2281	ttttttctgttaagactctctctcttgtaggaacgaataatgtctctctctgtagagctgggg	2340
Dh	2281	ttttttctgttaagactctctctctcttgtaggaacgaataatgtctctctctgtagagctgggg	2340
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Dh	2341	ctgcacagccttgagcggaggtctcggccgcttggtccgggagagcagtgctgataccgcgtccc	2400
Oy	2401	tccagccctctagaacgagatcctggtttcagctaaatgcaaggagaaactcaatgtttttta	2460
Dh	2401	tccagccctctagaacgagatcctggtttcagctaaatgcaaggagaaactcaatgtttttta	2460
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Dh	2461	agtttctttccctttaaagccctttttttaggcacatctgacagtcgtgtgggcggggaga	2520
Oy	2521	agataaggaaacatctcatcccttgctcgtctcatccagctgtgtgttaacatctcacggcca	2580
Dh	2521	agataaggaaacatctcatcccttgctcgtctcatccagctgtgtgttaacatctcacggcca	2580
Oy	2581	gaaccacacagatctgtctctggagagagctctggcaaggacatccctcatcacacatctgttgc	2640
Dh	2581	gaaccacacagatctgtctctggagagagctctggcaaggacatccctcatcacacatctgttgc	2640
Oy	2641	aaagtttaaaacaaaacaaaacaaaacaaaataaaataaaacaaaacaaaacaaaacccaa	2700
Dh	2641	aaagtttaaaacaaaacaaaacaaaacaaaataaaataaaacaaaacaaaacaaaacccaa	2700
Oy	2701	aaaaaaacaaaacaaaagagtcagccctcttgctctgtcttcaaaccccttaaaagaggagca	2760
Dh	2701	aaaaaaacaaaacaaaagagtcagccctcttgctctgtcttcaaaccccttaaaagaggagca	2760
Oy	2761	actccgtgagccttggtctcccgaggagagctcgtcgtcgtgaacctgggtccacagagacctg	2820
Dh	2761	actccgtgagccttggtctcccgaggagagctcgtcgtcgtcgtgaacctgggtccacagagacctg	2820
Oy	2821	ctttgttccccaagcatctgcaatagctgtgtgtttttagagctgtgggtctgtcgtcgtcgt	2880
Dh	2821	ctttgttccccaagcatctgcaatagctgtgtgtttttagagctgtgggtctgtcgtcgtcgtcgt	2880
Oy	2881	ggccaaagtgtgatagcagaggttttagaggtgtgtgtcacaaccccaatgacatctcagggccag	2940
Dh	2881	ggccaaagtgtgatagcagaggttttagaggtgtgtgtcacaaccccaatgacatctcagggccag	2940
Oy	2941	cggggggcgtgagcctcttcaggtccacggccagctgggcgtgttagcagatgtcgtctcct	3000
Dh	2941	cggggggcgtgagcctcttcaggtccacggccagctgggcgtgttagcagacatgtcgtctcct	3000

QY	3001	caagcagagggccagatgatcttcctcccttggttgcagcgtttccaaagccccgata	3061
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QY	3301	acattccagggcttgtaaatgtgtgataatgaaacattctcttaccctgttgabtgctag	3360
Db	3301	acattccagggcttgtaaatgtgtgataatgaaacattctcttaccctgttgabtgctag	3360
QY	3361	tgcgttaagatctcaactgtgtacaagcctggtttcattatcttgtaagaaaaacacagga	3420
Db	3361	tgcgttaagatctcaactgtgtacaagcctggtttcattatcttgtaagaaaaacacagga	3420
QY	3421	tcaattgataatcttgatgataataaatttgaataaacagattctc	3467
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RESULT 2

AA259132 standard; DNA; 3467 BP.

AC AA259132  
yy

DT 17-APR-2000 (first entry)  
XX

XX Phosphatase intracellular domain coding sequence.

cytosine phosphatase; antibody; thyroid cancer; ds.

XX WO9964591-A1  
PN

PD 16-DEC-1999.

'666T-N00-10  
XX

XX  
PA (FUSO) FISCO

PI Yamamoto H,  
YY

P-PSDB; MAY56

Antibody reco  
phosphatase L

Claim 4; Page

(P-subunit) of

the generation

[illegible]

QY 2041 cactgtgcccctctgtccacagaccacacttgagcccgcttcaagctctctgttgcgc 2100  
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 Db 2161 acatttaaggggttaaacgagagatttaagcctctccctctgatttctcttcgcga 2220  
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 Db 3001 cagagcaggggacagatgatttctccctggtttgagctgtttttaaagccccgata 3060  
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Db 3121 tatcaaatgtaacttaatacgtacctatataccacagctgtgaggggcagggagagcgc 3180  
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RESULT 3  
 AAA8739  
 ID AAA8739 standard; cDNA; 7702 BP.  
 XX  
 AC AAA8739;  
 XX  
 DT 19-FEB-2001 (first entry)  
 XX  
 DE Human protein tyrosine phosphatase PTP LAR cDNA.  
 XX  
 KW PTP LAR: protein tyrosine phosphatase; leukocyte antigen related;  
 KW human; epithelial cell; cell migration; cell proliferation; cancer;  
 KW antitumor; metastasis; antimetastatic; wound healing; vulnery;  
 KW diagnosis; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH  
 FT Key location/Qualifiers  
 FT CDS 371..6064  
 FT sig\_peptide /\*tag- a  
 FT mat\_peptide /\*tag- b  
 FT 419..6061  
 FT /\*tag- c  
 PN W0200061180-A2.  
 XX  
 PD 19-OCT-2000.  
 XX  
 PE 06-APR-2000; 2000MC-US09274.  
 XX  
 PR 09-APR-1999; 9905-0128673.  
 XX  
 PA (PLAC ) MAX PLANCK INST.  
 XX  
 PI Ullrich A, Muller T;  
 XX  
 DR WPI; 2000-647339/62.  
 DR P-PSDB; AAB19712.  
 XX  
 PT Treating a disease or a disorder characterized by epithelial cell  
 PT migration comprises administering a pharmaceutically acceptable  
 PT composition comprising PTP LAR -  
 XX  
 PS Disclosure: Fig 10-A-C; 107pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding human protein  
 CC tyrosine phosphatase PTP LAR (leukocyte antigen related), a  
 CC negative regulator of epithelial cell migration and tumour



0; Mismatches 0; Indels 0; Gaps 0;

Oy	4240	cgaacgtgaagagatctctctctctgcccacacccctctaaaccttgtagagatgvcggaagctca	64
Db	4240	cgaacgtgaagagatctctctctctgcccacacccctctaaaccttgtagagatgvcggaagctca	42399
Oy	65	ctacccagaccacgaagtatgtagagagaccacccaccccaatccccaatccacccctgcggagaca	124
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Oy	125	catcgagcgcctcccaagaccaaagatcgcgcctaaagtctccccaagagatatagtatccatcga	184
Db	4360	catcgagcgcctcccaagaccaaagatcgcgcctaaagtctccccaagagatatagtatccatcga	4419
Oy	185	cccttggaacagacagtcttcaacgttgtagagaaattcaaacctctgagatgtagaacagaccagaacg	244
Db	4420	cccttggaacagacagtcttcaacgttgtagagaaattcaaacctctgagatgtagaacagaccagaacg	4479
Oy	245	ctatgagaaatgctatcgcgcctctacgcgcacccctcgcagatataccttaacctctatcgatgcgt	304
Db	4480	ctatgagaaatgctatcgcgcctctacgcgcacccctcgcagatataccttaacctctatcgatgcgt	4539
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Db	4720	tgaatcaatctgtagccagcccgctgtagcccgagagaccctgtagccctattacatcagctgtaacctt	4779
Oy	545	ggacacagctgtagagctcgccgacacataatcgtctgcgaacctctgcacatccacaagaagtgcctc	604
Db	4780	ggacacacagctgtagagctcgccgacacataatcgtctgcgaacctctgcacatccacaagaagtgcctc	4839
Oy	605	cagctgaagaacgctgtagcctgcttcaagttctcaattcaatgacccgcggagacacatatgtagttcc	664
Db	4840	cagctgaagaacgctgtagcctgcttcaagttctcaattcaatgacccgcggagacacatatgtagttcc	4899
Oy	665	tgaatgataccaaatcccatccctcgcgcctctccctacgaacgggtcaaaagcctgcgaacccctcaga	724
Db	4900	tgaatgataccaaatcccatccctcgcgcctctccctacgaacgggtcaaaagcctgcgaacccctcaga	4959
Oy	725	cgacagggcccaatgtagtgcacatctcagcgcgggggttgtaggcgcgaacggcgtcgtctcaagt	784
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QY	785	gattatgacatgcttgtagagcggatgaaagacagaaagacggtgagcatctatgaccagct	844
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QY	845	gaccgcgacatgcatcacacacagagagaaatcacatggtgcagagacggagagacaaatgacgttcat	5079
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QY	1205	ggatgtgttatgaacagcaggaagggccctacatagctctacacaaagggagcctctgcagaaagagac	1264
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QY	1265	cgagagactctctgcgcacatgcacatgtgtagagacaaattccacacatccgtcatatgctgaccca	1324
Db	5500	cgagagactctctgcgcacatgcacatgtgtagagacaaattccacacatccgtcatatgctgaccca	5559
QY	1325	gcttcgggagagttggcagcgggagaaatgtgcacacaaatctgcccagagagcgctctgcctcg	1384
Db	5560	gcttcgggagagttggcagcgggagaaatgtgcacacaaatctgcccagagagcgctctgcctcg	5619
QY	1385	ctaaccaagtacttctgtctgaacccggatgctgtgagtatacaaatctgcgccagatatactctgcg	1444
Db	5620	ctaaccaagtacttctgtctgaacccggatgctgtgagtatacaaatctgcgccagatatactctgcg	5679
QY	1445	tgaattcaaaagttacagatgacccggatgtagcgtacaaagagacaaatcccgacagttccagttc	1504
Db	5680	tgaattcaaaagttacagatgacccggatgtagcgtacaaagagacaaatcccgacagttccagttc	5739
QY	1505	caacagactgtgcacagacagcggctgcacaaagaaacagcggagggatctcatctgacttcatcg	1564
Db	5740	caacagactgtgcacagacagcggctgcacaaagaaacagcggagggatctcatctgacttcatcg	5799
QY	1565	gcaaggtgtacataagacaaagagagcagttgtgacaaagatgtggccatctacacgttgtagccgacg	1624
Db	5800	gcaaggtgtacataagacaaagagagcagttgtgacaaagatgtggccatctacacgttgtagccgacg	5859
QY	1625	tgcctggtcgtgtggccgcacacgggggtgttctcatcaactctgagacatctgcctcctgagcgaatcg	1684
Db	5860	tgcctggtcgtgtggccgcacacgggggtgttctcatcaactctgagacatctgcctcctgagcgaatcg	5919
QY	1685	ctatgtagagggcgtgtgtgcagacatggtctcaagacgtgtgaagacccctgcgtgacacagcgcgcg	1744
Db	5920	ctatgtagagggcgtgtgtgcagacatggtctcaagacgtgtgaagacccctgcgtgacacagcgcgcg	5979
QY	1745	catgtgtcagacaaagaaacagatctcaagcgtgtgtctacacgttgcgtgcgcctgtgagtaacctcg	1804
Db	5980	catgtgtcagacaaagaaacagatctcaagcgtgtgtctacacgttgcgtgcgcctgtgagtaacctcg	6039
QY	1805	cagcttggacacacatgtgcaacgttgtaactacgctctccctctcctccgcaaccccgccggt	1864
Db	6040	cagcttggacacacatgtgcaacgttgtaactacgctctccctctcctccgcaaccccgccggt	6099
QY	1865	gggctccggagggagacacagctctcctctgtagccatactcgacacatcgctccagcctcctctacg	1924

```

db 6100 gggctcggagggagaccagctcctctgagccatccagacatcgtccagccctctcaga 6159
Oy 1925 cagatgtcgtctactcgtgcagagcaagcccaaggagatccacagctttcaaggagcttgc 1984
Db 6160 cagatgtcgtctactcgtgcagagcaagcccaaggagatccacagctttcaaggagcttgc 6219
Oy 1985 acacaaatcagagagagcctaaacatccctggggaagtgtgagcccaagcaagcaact 2044
Db 6220 acacaaatcagagagagcctaaacatccctggggaagtgtgagcccaagcaagcaact 6279
Oy 2045 gtggccctctctcaccagcaagcccaagccctcagagctctgttctgtgtcc 2104
Db 6280 gtggccctctctcaccagcaagcccaagccctcagagctctgttctgtgtcc 6339
Oy 2105 gcaattcctcagctctctcagagctctcagagctctcagagctctcagagctctc 6399
Db 6340 gcaattcctcagctctctcagagctctcagagctctcagagctctcagagctctc 6399
Oy 2165 taagtgaggtagacatgagagatcttagcctctcctcctcagagctctcagagctctc 2224
Db 6400 taagtgaggtagacatgagagatcttagcctctcctcctcagagctctcagagctctc 6459
Oy 2225 gtaatcgcagagagagcagcagctgtgagagctgtgagagctgtgagagctgtgag 2284
Db 6460 gtaatcgcagagagagcagcagctgtgagagctgtgagagctgtgagagctgtgag 6519
Oy 2285 ttctgtatgactctcgtcagagagcaagaaatctgctcctcctcagagctgtgagagct 2344
Db 6520 ttctgtatgactctcgtcagagagcaagaaatctgctcctcctcagagctgtgagagct 6579
Oy 2345 cagcctcgcagagagagcagcagctgtgagagctgtgagagctgtgagagctgtgag 2404
Db 6580 cagcctcgcagagagagcagcagctgtgagagctgtgagagctgtgagagctgtgag 6639
Oy 2405 gccctcagagagagatccctgttccagctaaatgcaagagaaatcagagctgttccag 2464
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Oy 2465 ttgttccctccttaaaagccttttttaagcccaatcagagctgtgagagagagagat 2524
Db 6700 ttgttccctccttaaaagccttttttaagcccaatcagagctgtgagagagagagat 6759
Oy 2525 agggaaacatcactccctgtcgtctcactccagctgtgtgttcaacatccagccagac 2584
Db 6760 agggaaacatcactccctgtcgtctcactccagctgtgtgttcaacatccagccagac 6819
Oy 2585 cacaagatgtctcgtgagagagcctgtcgaagcattccatcaacatcgttctgcaag 2644
Db 6820 cacaagatgtctcgtgagagagcctgtcgaagcattccatcaacatcgttctgcaag 6879
Oy 2645 ctataacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 2704
Db 6880 ctataacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 6939
Oy 2705 aaaaaaaagagagagcctcctgtgctcctcctcctcctcctcctcctcctcctcctc 2764
Db 6940 aaaaaaaagagagagcctcctgtgctcctcctcctcctcctcctcctcctcctcctc 6999
Oy 2765 cgtgtgctcgtgagagcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 2824
Db 7000 cgtgtgctcgtgagagcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 7059
Oy 2825 ggtcccgagcctcagatagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2884
Db 7060 ggtcccgagcctcagatagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7119
Oy 2885 aagtgatagcagagctgagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2944
Db 7120 aagtgatagcagagctgagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7179
Oy 2945 ggcgtgctgagccttcaagctcagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3004

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Db 7180 ggcgtgctgagccttcaagctcagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7239
Oy 3005 gcaaggagcagagatcttctcctcctcctcctcctcctcctcctcctcctcctcctc 3064
Db 7240 gcaaggagcagagatcttctcctcctcctcctcctcctcctcctcctcctcctcctc 7299
Oy 3065 ctctttccatcccaagatgacctcctcctcctcctcctcctcctcctcctcctcctc 3124
Db 7300 ctctttccatcccaagatgacctcctcctcctcctcctcctcctcctcctcctcctc 7359
Oy 3125 aatgtaactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 3184
Db 7360 aatgtaactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 7419
Oy 3185 tccctcgtcagcagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 3244
Db 7420 tccctcgtcagcagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 7479
Oy 3245 tagctgagagagctgtgtcgcagctcctcctcctcctcctcctcctcctcctcctcct 3304
Db 7480 tagctgagagagctgtgtcgcagctcctcctcctcctcctcctcctcctcctcctcct 7539
Oy 3305 tccagagctgtgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3364
Db 7540 tccagagctgtgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7599
Oy 3365 gtaagatcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3424
Db 7600 gtaagatcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3479
Oy 3425 tgcataatctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7660
Db 7660 tgcataatctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7702

RESULT 4
AAZ91908
ID AAZ91908 standard; DNA; 7702 BP.
XX
AC AAZ91908;
XX
DT 07-JUN-2000 (first entry)
XX
DE Human protein tyrosine phosphatase, LAR, coding sequence.
XX
KW Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR;
KW CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;
KW non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;
KW heart disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200002922-A1.
XX
PD 20-JAN-2000.
XX
PF 06-JUL-1999; 99WO-JP03656.
XX
PR 10-JUL-1998; 98WO-JP03120.
XX
PA (FUSO ) FUSO PHARM IND LTD.
XX
PI Yamamoto H, Tsujikawa K, Uchino Y;
XX
DR WPI: 2000-182215/16.
XX
DR P-PSDB: AA81785.
XX
PT Antibody for diagnosis and treatment of insulin resistance disorders
PT and syndrome X recognises the intracellular domains of tyrosine
PT phosphatase
XX
PS
XX
Example 1; Page 61-77; 83pp; Japanese.

```

SV sequence 7702 BP; 1636 A; 2286 C; 2292 G; 1488 T; 0 other;

[illegible]

65 ctacccgagcgcctccatctctcgaccctgtgagatcgcgagctcaa 4299

4355 caccagaccccggtatgcgagaccaccaccatcccatcaccgacctgcgacaa 4359

4360 catcgagcgcttcaaaagccacgatgctgctcaagtctctccagagatgatgattccatcga 4419

4420 ccctgacgcagttcacgtgagaaattcaacctggaggttaacaaagcccaagaaaccc 4470

[illegible]

b  
4540 cccgggagtgaactacatcaataaccacactacaattccttgcagaaaggccca 364

[illegible]

|||||  
4560 ACATCCCACTGCTGAGGAGAACTCCCGGTAAATG 484

4730 |||||cagccctgacacgagacctgtgacctattcagtgacctgt 544

545 ggacacagctggagctggccacatacaactgtgcgaccttcgcactccacaagagtgctc 604

605 cagtgaagcgtgagctgcgtcagttcagltcatgacctgacccaagcatgaattcc 664

665 tgaatccaactcccatctgaccttctctacacagqtcnaagcctnnaaacctata-- 704

**725** cgcagggcccatgctgtcactgcacaaacaaaatctaaccaaaaaataatga  
-----gcgcgcacccccccataga 4959

785 gattgataccatattomacccaataaa  
5019

845 GACCTGATGAGTGGTTGCGTCGAGGAGACGCGAGGAGACGTCGACATCTATGTGCCAAGT 5079

100

905 ccattagagcgtctgtgagagctgccaagctgcgcgcacacagaagatgacctgacccgcgaacct 964

965 gtagccacatcagaagctgycgaagtgccttcagaaagaaatattcccccaat--

QY 1025 gctcgaattcaagttgcttgaccacactccaaacccccacacat-  
35259

1085 cctgaccttcacacaaatctctctctccacacgctccccgcgttcattcatcgagcnaa 5319

0x 1145 ttttccccccgctgttgacaatcatgccctaagattgaccgcg 5379

5439

5440 ggatggtatagacagcagaagcctacatagctaacacgagcctctgacagaaacac 5499

5500 cgaggaactctgcgcatagtctatgaggagacaattccaccatcatcgatcatcattccaa 5550

[illegible]

b  
5620 ctaccagtaacttqtlqttaacccatatactcatttcgcaaaacggccccgcatactctcg 1444

5680 tgaattcaaatcaccgaatccccccagcttc 1504

|||||  
|||cgcagacgagcgccggcgaaggatctgtacttcattgcgcg 1564  
|||caaacaaatacccccccgaagaacacgacggagtgacgggagcg 5740  
|||||

gcaaggcattgacagatggcctatcacggtgacatgcag 1624

1625 tgcctgcgtggccgcacccgggtgtttcatcactctgagcatcgttcctgagcgcacatcgc 1684

1685 ctatgaggcgctgtgcacatgtttcagaccgtgaagaccctcgtacacacacatctcttc 1744

1745 catgtgacagacagaccagtatcaacttctqclaccafatacggccgcctggaatttttgctg

1805 cagcttgaccacatatgcagaatgaactaaccaaatcccatcatttccg 6039

1865. qqqtcccccccccccccccccccccccccccccccccccgccgctgg 6099

[illegible]

6219

Oy	3065	ctctttccacatcccaagatgcccctctaaaccagttgttggcagagactactgtgactctatc	3125
Db	7300	ctctttctccactcccaagatgcccctctaaaccagttgttggcagagactactgtgactctatc	7335
Oy	3125	aatgttaactctaaatcagttcccttaatacccaagcttgcgtgaagggcagagagagcctct	3185
Db	7360	aatgttaactctaaatcagttcccttaatacccaagcttgcgtgaagggcagagagagcctct	7410
Oy	3185	tctctctgggcagcgctatcatalagatgaatgttgagggggggagaggtgtcacaagctgtt	3245
Db	7420	tctctctgggcagcgctatcatalagatgaatgttgagggggggagaggtgtcacaagctgtt	7475
Oy	3245	tagctgaaggagacgttggtggtccgaaggtccccaaccttagctagaatgtcaagatcaacct	3300
Db	7480	tagctgaaggagacgttggtggtccgaaggtccccaaccttagctagaatgtcaagatcaacct	7535
Oy	3305	tcccaaggttggtaaatgtttggaatgaagaacatccaatttcaactttgttgaatgctcagtgtc	3365
Db	7540	tcccaaggttggtaaatgtttggaatgaagaacatccaatttcaactttgttgaatgctcagtgtc	7595
Oy	3365	gtagagttccaatgtttgacacagttcgtttcattttgtttaagaanaaacataagacat	3425
Db	7600	gtagagttccaatgtttgacacagttcgtttcattttgtttaagaanaaacataagacat	7655
Oy	3425	tgtcataattcttgatggttaataaatgtgaataatgcagatttt	3467
Db	7660	tgtcataattcttgatggttaataaatgtgaataatgcagatttt	7702

... other;

D	5260	gctcaggtctcaagattgcctcgcgcacagctctccaaagcgcacacgcctccgcctctcatcagccgca
Q	1085	ccctgcgcctctccaaacaaagttccaaagaccgcctcgtgtgaacatactatgcctctacgaattagcccg
D	5320	ccgcgcgcgcgaacaaagtctcaagaaaccgcctcgtgtgaacatactatgcctctacgaattagcccg
Q	1145	tgtgtgtcctcagaccctaccgcctcgtgtgtgaaggcctctgaatacaatactgcacgtctcct
D	5380	tgtgtgtcctcagaccctaccgcctcgtgtgtgaaggcctctgaatacaatactgcacgtctcct
Q	1205	ggatggttatagaaagaaagaaagcctcaataagctatacagaaggccctctgcagaaagaaac
D	5440	ggatggttatagaaagaaagaaagcctcaataagctatacagaaggccctctgcagaaagaaac
Q	1265	cgaagactcttcgcgcacatgctaattggaacatacttccacatactatctcagatgcgaacaa
D	5500	cgaagactcttcgcgcacatgctaattggaacatacttccacatactatctcagatgcgaacaa
Q	1325	gctctggagaaatcgcgcagagaaagaaatccaccacgcctcgcgcagagaaagcgcctgtcgc
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D	5620	ctccaccagctacttctgttctgttcaccgaatgcctcgtgtacaaagatacgcctcagatattctcgc
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D	5680	tggattccaagatcagcagatagccgcgggtctgcgcgtctcaagaaatactccgcagattccagct
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D	5740	caacagaactgcgcacagaaagaaagcgtctgcacaaagaaagcgaagaaatctatctatctacgc
Q	1565	gaaagtgtgataaagaaagaaagaaagcaagtttggacaaagatcgggcctatacagttgacatagag
D	5800	gaaagtgtgataaagaaagaaagaaagcaagtttggacaaagatcgggcctatacagttgacatagag
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D	5920	ctatagaaagcgttcgtcgaatattcttcagaacccgttgaagaaaccctcgcctgaacacgcctcgc
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D	5980	catgctgcacagaacagaagcagacagatactacgcctcgtctcaccgttcgggcgcctcgcgaattac
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D	6040	cagctcttgacacatactgaagaaagttaactacacgcctccctcctccgcacacacccgcgcgt
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D	6100	ggagctcgcgaagaaagaaacacacctcctcctgaagcatacgaacacatcgtctccagcctccctacg
Q	1925	cagatgcctcactatcgcgaagcacaagcccaacgggatacaagaagcttccagaaacgttcgc
D	6160	cagatgcctcactatcgcgaagcacaagcccaacgggatacaagaagcttccagaaacgttcgc
Q	1985	acacacatactgaagctcgaagacatcccttcgcgaagtgcgaattgcgcacaaagacagagcagact
D	6220	acacacatactgaagctcgaagacatcccttcgcgaagtgcgaattgcgcacaaagacagagcagact
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D	6280	gtggccctctcttccacaaagaccacacacttggagaccgcctccaaagcctctgtctgcctcc
Q	2105	gcaattctcagctctctctcatatgagttgaggttgcgaatgcctctcctcgtctgcctcc

Db 6340 gaattctcaatgcttctctcaatgaggttggtgggcaagcctcctttaaatacat 6399  
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 Db 6400 taagtgggtagaactgagggaattttagcctctcccttgatcttctcttcgcaatcc 2224  
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 Db 7120 aaggtgaatgacagaggttaggtgtgtgtgacacacacacacacacacacacacacac 2944  
 Oy 2945 ggcgtggtggtcctttagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3004  
 Db 7180 ggcgtggtggtcctttagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3004  
 Oy 3005 gcaaggagcagatgatttctcctcgtgttgacagcagcagcagcagcagcagcagcagc 3064  
 Db 7240 gcaaggagcagatgatttctcctcgtgttgacagcagcagcagcagcagcagcagcagc 3064  
 Oy 3065 cctcttccactcagaatgctcctcataaacaatgtgcaagagcagcagcagcagcagcagc 3124  
 Db 7300 cctcttccactcagaatgctcctcataaacaatgtgcaagagcagcagcagcagcagcagc 3124  
 Oy 3125 aatgtgacttaactagcctcctatacccaatgtgcaagagcagcagcagcagcagcagc 3184  
 Db 7360 aatgtgacttaactagcctcctatacccaatgtgcaagagcagcagcagcagcagcagc 3184  
 Oy 3185 tctctcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3244  
 Db 7420 tctctcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3244

Oy 3345 taagtgggagcgtgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 3304  
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 Oy 3305 tccaggttggttaagtgtgtagatgaataatcttcttcttcttcttcttcttcttcttct 3364  
 Db 7540 tccaggttggttaagtgtgtagatgaataatcttcttcttcttcttcttcttcttcttct 3364  
 Oy 3365 gtagagttacgtgtgtgtagacagctgttcttcttcttcttcttcttcttcttcttctt 3424  
 Db 7600 gtagagttacgtgtgtgtagacagctgttcttcttcttcttcttcttcttcttcttctt 3424  
 Oy 3425 tgcataatcttgatgataataatgataatgataatgataatgataatgataatgataat 3467  
 Db 7660 tgcataatcttgatgataataatgataatgataatgataatgataatgataatgataat 3467

RESULT 6  
 ID AAF15575 standard; CDNA: 3064 BP.  
 AC AAF15575;  
 XX  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 XX  
 DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:10.  
 XX  
 KW Human: prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KW neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;  
 KW vulnery; gastrointestinal; nephrotoxic; anti-infective; gynecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055174-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US05988.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI (ROSE/) ROSEN C A.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 WP: 2000-587513/55.  
 DR P-PSDB: AAB56372.  
 XX  
 PT Prostate cancer associated gene sequences, referred to as prostate  
 PT cancer antigens, useful for treatment, prevention, and diagnosis of  
 PT disorders such as prostate cancer -  
 XX  
 PS Claim 1: Page 621-622; 2338bp; English.  
 XX  
 CC AAF15566 to AAF16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
 CC The prostate cancer antigens can have neuroprotective, cytosolic,  
 CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,  
 CC nephrotoxic, anti-infective, gynecological and antibacterial activities,  
 CC and can be used in gene therapy. The prostate cancer antigen  
 CC polynucleotides may be used for detection of prostate cancer, chromosome  
 CC identification, as chromosome markers, and for numerous other diagnostic  
 CC or research purposes. The prostate cancer antigens may be used to treat  
 CC disorders such as neural, immune, muscular, reproductive,  
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative.  
 CC disorders, wounds, and infectious diseases. AAF15566 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention.



XX Sequence 3064 BP; 695 A; 820 C; 845 G; 700 T; 4 other:  
SQ

Query Match: 84.1%; Score 2914.4; DB 21; Length 3064;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 2960; Conservative 1; Mismatches 3; Indels 25; Gaps 2;

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OY 561 gccacatacactgtgacacctctgcacctacacaaagtggtccacagtgaaagcgtag 620  
DB 61 gccacatacactgtgacacctctgcacctacacaaagtggtccacagtgaaagcgtag 620  
OY 621 ctgctgtacagttcagttcagttcagttcagttcagttcagttcagttcagttcagttc 680  
DB 121 ctgctgtacagttcagttcagttcagttcagttcagttcagttcagttcagttcagttc 680  
OY 681 atccgtgacctctctacacagtggtcagagctgtcagacacctctctctctctctctct 740  
DB 181 atccgtgacctctctacacagtggtcagagctgtcagacacctctctctctctctctct 740  
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DB 241 gtgcactgtgacgagcggtgtgacgacgacgacgacgacgacgacgacgacgacgacg 800  
OY 801 gagcggtatgaaagcagagaaagcgtgtgacatctatgtcagacgtgtcagacgacgac 860  
DB 301 gagcggtatgaaagcagagaaagcgtgtgacatctatgtcagacgtgtcagacgacgac 860  
OY 861 cagaggaactacatgt 920  
DB 361 cagaggaactacatgt 920  
OY 921 gagcgctgacgagcggt 980  
DB 421 gagcgctgacgagcggt 980  
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DB 481 aagctgtgacgagcggt 1040  
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DB 601 ttcacgaacacgagctgt 1160  
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DB 1141 accggt 1700  
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DB 1801 ttcctcattgt 2360  
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DB 1861 ggcgt 2420  
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DB 1921 ggcgt 2480  
OY 2481 ggcgt 2540  
DB 2519 ggcgt 2540





Oy 1649 gtccacatcctcgagcatcgtctctgagagcatgcgtctatgagcgctggtctcgacattgt 1706  
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 Oy 1709 tcagacgcgtgaagagacctcgctgtatacagcgtctctgccaatgctgacaacagagaccata 1766  
 Db 5638 tcagacgcgtgtgaagatgctctaacgaaccccgcgcgccatctgtgcagacagagtgatga 5697  
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 Db 5698 ccagctctgttatccagcagcgacatcgagatccctcggaaagcttgcaccactatgacactta 5757  
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 Db 5758 aagccatgctcccccccgagcccggaacac 5786

[illegible]

Query Match	37.1%	Score 1285;	DB 18;	Length 6000;
Best Local Similarity	81.4%	Pred. No. 2.1e-271;		
Matches 1489; Conservative	0;	Mismatches 340;	Indels 0;	Gaps 0;

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QY	1169	tgtgtgagagcctctgtaatacatcaaatcccgcttccctggatgtgttgaacagcgaagagac	1228
Db	5098	tgtgtgagagcctctgtaatacatcaaatcccgcttccctggatgtgttgaacagcgaagagac	5157
QY	1229	ctatacagatcaacacagggggccctctgcaagagaacacgaagaaatctctgtgccaatgata	1288
Db	5158	ctatacagatcaacacagggggccctctgcaagagaacacgaagaaatctctgtgccaatgata	5217
QY	1289	ggagacaacattccacacatcatcgtatctgatacgaacagcttcggagatctggagatggcagggagaa	1348
Db	5218	ggagacaacattctgaacatcgtgtgtgtatgtctgtacccaagctctggagagatggcagggagaa	5277
QY	1349	atgccaacacagctctgccaagacagagagcctctgtctcgcatacagaatactctgtgtgaaccc	1408
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QY	1409	gattgctctgaattacaacacatgcccacgaattatattctgctgtgagttccaagatccaagatgacgg	1468
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QY	1469	ggatgtggcagattcaagagaaacatccgacagttccagttccaaagatctggccagagacagggcgt	1528
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QY	1529	ggccaacacagcggagagatctcatctgtaacttccagcttcacggcagagtgtaaaagacacaaagagca	1588
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QY	1649	gttatacactctgaagatcgtctcctctggaagcgaatgacgtatagtgaagacgtgtgtgtgaacgtt	1708
Db	5578	gttatacactctgaagatcgtctcctctggaagcgaatgacgtatagtgaagacgtgtgtgtgaacgtt	5637
QY	1709	tcaagacccgtgaagacccctgctgtatcaagagctctctgcatgtgtgacgaacaaagaggaacgtta	1768
Db	5638	tcaagacccgtgtgaagatgctatcgaacccacgaagcggcgccaaatgtgtgacgaacaaagaggaacgtta	5697
QY	1769	tcaagcgtgtcatcgtgtgacccctctggaatctggaatcctggaacgtcttgacacatttgaaagta	1828
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Location/Qualifiers
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sequence 6000 BP; 1229 A; 1971 C; 1803 G; 997 T; 0 other;

②

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Db	4558	gttccagatttaagcgtgtgcgcgtgcagacataagcgtgtgcgcgaataaccacagctctctcgcg	4617
Oy	689	cttcctacgaacggttcaagagccttgcaaaccccccataagacagaaagggccatctgtgtgtgacctg	748
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Oy	749	caagctgcggcgtgtgcgcgcacgcgtgtcttcatcgtgtgataatgacatgtgtgtgagcgagat	808
Db	4678	caagtgcgcgtgtgtgcgcgcacagcgtgtgtcttcatctgtacacgcctacgtctgtgcgcgtat	4737
Oy	809	gaagcagcggaaagacggtgtgacatctatgacacagctgtgacgtgcatagtgataccagagaa	868
Db	4738	caagccacagaaagaaagacgtctgtatgtctatgtgcacacgttgacgtctactgtgtgtgtccgcaca	4797
Oy	869	ctacatagttgacagacgagagacacagatgaagtgttcatccatagaagcgtctgtcttgaaagctgc	928
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Oy	1109	ccggtcgtgtgtgaacatactgacctacaaatctgaacccggtgtgtgtctgcagggccatctcgtgtg	1168
Db	5038	ccgcgcgtgtgtgaacatactgacctacaaatctgaacccggtgtgtgtgtctgcagggccatctcgtgtg	5097
Oy	1169	tgtgtgaggggtcctgtgactacatacgaatgagcagctctctctgtgatagtttatagaacagagaaagtc	1228
Db	5098	tgtgtgaggggtcctgtgactacatacgaatgagcagctctctctgtgatagtttatagaacagagaaagtc	5157
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Oy	1589	gtttgcgcacaaagatgtggcctatccagttgacatgcagatgtctgtgcgtgtggcgcgcagcggggt	1648
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[illegible]

```

RESULT 11
AA094311 ID AA094311 standard; cDNA to mRNA; 4555 BP.
AC XX AA094311;
XX 10-MAY-1996 (first entry)
DE Tyrosine phosphatase MPP-delta cDNA.
KW Tyrosine phosphatase MPP-delta; murine; brain tissue;
KM glutathione-S-transferase; fusion protein; E. coli; differentiation;
KW activation; information transmission; nervous system; immune system;
OS carcinogenesis; ds.
XX Mus musculus domesticus.
XX Key Location/Qualifiers
FH 1..477
FT FT 5'UTR /tag= a
FT CDS 478...4353 /tag= b
FT /product= MPP-delta
FT 3'UTR 4354...4555 /*tag= c
PN JP07236487-A.
XX 12-SEP-1995.
PD 28-FEB-1994; 94UP-0054726.
XX 28-FEB-1994; 94UP-0054726.
PR 28-FEB-1994; 94UP-0054726.
XX (TOKS-) TOKYOTO SHINKEI KAKAKU SOGO KENKYUSHO ZH.
PA MPI: 1995-347455/45.
XX P-PSDB: AAR75201.
DR DNA encoding tyrosine phosphatase MPP delta - useful for
XX elucidation of signal transduction mechanisms.
PT Claim 1; Page 5-11; 14pp; Japanese.
PS This sequence represents the tyrosine phosphatase MPP-delta coding
CC sequence. This sequence was isolated from murine brain tissue and
CC was cloned, for expression, into the downstream region of a
CC glutathione-S-transferase sequence and expressed as a fusion protein
CC in E. coli. MPP-delta proteins regulate differentiation and
CC activation of cells. This sequence can be used in the elucidation of
CC the molecular mechanism for information transmission in cells,
CC regulation mechanisms in the nervous system or immune system, or in
CC the mechanism of carcinogenesis.
SO Sequence 4555 BP; 1374 A; 966 G; 1032 C; 1163 T; 0 other:

Query Match 30.5%; Score 1059; DB 16; Length 4555;
Best Local Similarity 75.28; Pred. No. 5.1e-222;
Matches 1362; Conservative 0; Mismatches 440; Indels 9; Gaps 3.

Dy 29 ccactctcgcgacccgtgagatgcggaagtcacaactcacgagccccagtatggaga 88
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Oy 89 ccacccacccatcccacacgacctggcggaacacatcgagcgccccaagacaaga 148
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Oy 149 tggccccaagttccccaagagatgagatcatcgaccctggagcagcagttcaagtggga 208
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 Oy 1289 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1348  
 Db 3816 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1387  
 Oy 1349 atgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3875  
 Db 3876 atgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1408  
 Oy 1409 gatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3935  
 Db 3936 catgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1468  
 Oy 1469 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3995  
 Db 3996 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1528  
 Oy 1529 gcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4052  
 Db 4053 gcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1588  
 Oy 1589 gttggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4112  
 Db 4113 gttggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1648  
 Oy 1649 gttggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4172  
 Db 4173 gttggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1708  
 Oy 1709 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4232  
 Db 4233 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1768  
 Oy 1769 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4292  
 Db 4293 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1828  
 Oy 1829 actaacgctcc 1839  
 Db 4353 gaaaccccttc 4363

Oy 1289 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1348  
 Db 3816 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1387  
 Oy 1349 atgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3875  
 Db 3876 atgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1408  
 Oy 1409 gatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3935  
 Db 3936 catgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1468  
 Oy 1469 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3995  
 Db 3996 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1528  
 Oy 1529 gcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4052  
 Db 4053 gcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1588  
 Oy 1589 gttggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4112  
 Db 4113 gttggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1648  
 Oy 1649 gttggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4172  
 Db 4173 gttggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1708  
 Oy 1709 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4232  
 Db 4233 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1768  
 Oy 1769 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4292  
 Db 4293 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1828  
 Oy 1829 actaacgctcc 1839  
 Db 4353 gaaaccccttc 4363

RESULT 12  
 AAX24802 standard; DNA: 1029 BP.  
 AAX24802:  
 21-JUN-1999 (first entry)  
 Leukocyte antigen related protein tyrosine phosphatase domain DNA.  
 Leukocyte antigen related protein tyrosine phosphatase; LAR1;  
 human; T7 promoter; operator; gene expression; vector; pZRV3.3;  
 OS Homo sapiens.  
 PN MO905297-A1.  
 PD 04-FEB-1999.  
 PF 21-JUL-1998; 98MO-G802175.  
 PR 25-JUL-1997; 97GB-0015660.  
 PA (ZENNE) ZENNECA LTD.  
 PI Bunde11 KR, Hockney RC, Kara BV, Plo11 D;  
 DR WPI; 1999-142947/12.  
 XX New system for expression of recombinant proteins - comprises a T7



PT based promoter-driven expression system having upstream and  
 PT downstream operator sequences  
 PS  
 XX  
 XX Disclosure; Page 28; 56pp; English.

CC This DNA sequence encodes the leukocyte antigen related protein  
 CC tyrosine phosphatase domain 1 (LAR1, aa1275-1613). The DNA was  
 CC subcloned as a NheI-BglII fragment between the NheI and BamHI  
 CC cloning sites of vector pET11a and of novel, claimed vector  
 CC p27#13.3, which has a novel 77 based promoter-driven expression  
 CC system that utilizes upstream and downstream operator (pPOP)  
 CC operator (pPOP) sequences. Expression studies in E. coli hosts  
 CC demonstrates the poor performance of pET11a in terms of high basal  
 CC expression. The new 77 promoter-based expression system provides  
 CC improved control of expression and improved levels of protein  
 CC expression. Basal expression in the absence of inducer can be  
 CC reduced to a level which permits the cloning and expression of  
 CC toxic gene products. The system also allows control of production  
 CC of heterologous proteins in an inducer concentration-dependent  
 CC manner over a wide range of expression levels.  
 XX  
 XX Sequence 1029 BP; 236 A; 316 C; 286 G; 191 T; 0 other;

Query Match 28.0%; Score 970; DB 20; Length 1029;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-203;  
 Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 cggactgaaggagctctctgtgagcagctctgagcctgtgagatgagagcctca 64  
 DB 48 cggactgaaggagctctctgtgagcagctctgagcctgtgagatgagagcctca 64  
 OY 65 ctaccagaccaggtatgagagagcagcaccacccatcccatccagcagctgagaca 107  
 DB 108 ctaccagaccaggtatgagagagcagcaccacccatcccatccagcagctgagaca 124  
 OY 125 catcagagcctcaagaagcagatgagcctcaagttccagagagatgagcctca 167  
 DB 168 catcagagcctcaagaagcagatgagcctcaagttccagagagatgagcctca 184  
 OY 185 cccctgagcagagctcagtgagagaaattcaaacctgagagtgagaaagcccaaaacg 227  
 DB 228 cccctgagcagagctcagtgagagaaattcaaacctgagagtgagaaagcccaaaacg 244  
 OY 245 ctatgagagatgagcagcagcagcctctgagagcagcctctatctatgagcgt 287  
 DB 288 ctatgagagatgagcagcagcagcctctgagagcagcctctatctatgagcgt 304  
 OY 305 ccccgagagtgagctacataatgcaactacatgagcagcagcctctatctatgagcgt 347  
 DB 348 ccccgagagtgagctacataatgcaactacatgagcagcagcctctatctatgagcgt 364  
 OY 365 catcgcagcagagggccctctgagagagcagcagcagcagcagcagcagcagcagc 407  
 DB 408 catcgcagcagagggccctctgagagagcagcagcagcagcagcagcagcagcagc 424  
 OY 425 acagcgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 467  
 DB 468 acagcgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 484  
 OY 485 tgatcagctacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 527  
 DB 528 tgatcagctacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 544  
 OY 545 ggaacagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 587  
 DB 588 ggaacagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 604  
 OY 605 cagtgagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 647  
 DB 648 cagtgagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 664  
 OY 665 tgaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 707  
 DB 707 tgaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 724

DB 708 tgaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 767  
 OY 725 cgcagggccatggtgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 784  
 DB 768 cgcagggccatggtgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 827  
 OY 785 gattgatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 844  
 DB 828 gattgatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 887  
 OY 845 gacctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 904  
 DB 888 gacctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 947  
 OY 905 ccatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 964  
 DB 948 ccatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1007  
 OY 965 gtagccac 974  
 DB 1008 gtagccac 1017

RESULT 13  
 AAA44322 standard; cDNA; 601 BP.  
 AAA44322;  
 21-AUG-2000 (first entry)  
 Human secreted expressed sequence tag SEQ ID NO:897.

Human: mouse; chicken; rat; secreted expressed sequence tag; SESN;  
 expressed sequence tag; EST; probe; chemotactic; proliferative;  
 immunomodulatory; hematopoietic; chemokine; analgesic; hemostatic;  
 thrombolytic; antiinflammatory; cytosolic; antibacterial; antitumor;  
 antiviral; antidiabetic; antistaphylococcal; antiparkinsonian;  
 anticancer; osteoprotective; neuroprotective; nociceptive; antiparkinsonian;  
 vaccine; osteoprotective; anticonvulsant; antidepressant; gene therapy;  
 insulin dependent diabetes; multiple sclerosis; allergic condition;  
 lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;  
 central nervous system disorder; Alzheimer's disease; stroke;  
 Parkinson's disease; Huntington's disease; coagulation disorder;  
 haemophilia; thrombosis; inflammatory disorder; Crohn's disease;  
 tumour; infection; depression; psoriasis; ss.

Homo sapiens.  
 WO200021991-A1.  
 20-APR-2000.  
 15-OCT-1999; 99WO-US24206.  
 15-OCT-1998; 98US-0104436.  
 (GENM) GENETICS INST INC.

PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Werberg D, Treacy M, Bowman MR;  
 DR WPI: 2000-317938/27.

Isolated polynucleotides, and encoded proteins, comprising secreted  
 PT expressed sequence tags (ESTs), useful for treating various disorders  
 PT such as autoimmune, infectious, and central nervous system disorders -  
 XX  
 XX Claim 1; Page 433; 803pp; English.

AAA443426 to AAA45925 represent specifically claimed secreted expressed

[illegible]

ID	AA021001	standard; DNA; 2872 BP.
AC	AA021001;	
DT	28-MAY-1992	(first entry)
DE	Murine receptor-type protein tyrosine phosphatase gene.	
XX		
XX	R-PTPase; cellular metabolism; cancer; diabetes; mouse; ss.	
OS	Mus musculus.	
XX		
XX	Key	Location/Qualifiers
FT	CDS	259..2640
FT		/**tag= a
XX		
PN	MO9201050-A.	
XX		
PD	23-JAN-1992.	
XX		
PF	11-JUL-1991; 91MO-US04892.	
XX		
PR	26-FEB-1991; 91US-0654188.	
PR	11-JUL-1990; 90US-0551270.	
XX		
PA	(UYNY-) NEW YORK UNIV.	
XX		
PI	Schlessinger J;	
XX		
DR	WPI; 1992-056865/07.	
XX	P-PSDB; AAR20743.	
PT	Human receptor-type protein tyrosine phosphatase - has DNA	
XX	encoding it and antibodies specific for it, useful for screening	
XX	drugs affecting R-PTPase activity, and detection of mutant genes	
PS	Claim 7; Fig 1; 77pp; English.	
CC	The sequence is that of the gene encoding mouse receptor-type	
CC	protein tyrosine phosphatase (R-PTPase). It may be used to produce	
CC	the R-PTPase recombinantly. Probes may be designed from the gene	
CC	that can be used to detect mutant genes in PCR amplification and	
XX	hybridisation assays.	
XX		
SO	Sequence 2872 BP; 785 A; 721 C; 724 G; 642 T; 0 other;	

ID	Key	Location/Qualifiers
DB 162	agtcgtgctggtgcccagccggggtgtcatcactctgtgcatcgtctctgagcgatg	1682
DB 2428	atgcctccggggcagagcagcaggaaccttcgtgaccttgagcagctctggaacgtgtg	2487
QY 1683	cgctatgagggcgtgtgtctgcatatgtttcagacccgttgaaagccctgcgtacacgctct	1742
DB 2488	aaagcagaagaagatcttcagatgtcttcacaaatcgtcacagagccctgcgtgagagccca	2547
QY 1743	ggcctagtgagcagacagagaccagctgctgctacgctgagcggccctgagatccct	1802
DB 2548	cacatagctgcagacacagcagacagatgatctctgctacaaaggctgtacaggaatcatc	2607
QY 1803	ggcagcttgcagccactgcga	1824
DB 2608	gagccttccagatcatgcga	2629
RESULT 15		
AAT36881	AAT36881 standard; cDNA; 2872 BP.	
AC XX	AAT36881;	
XX XX	22-OCT-1996 (first entry)	
DT XX	Murine receptor type protein tyrosine phosphatase alpha cDNA.	
DE XX	Murine; mouse; receptor type; tyrosine phosphatase alpha;	
KW KM	brain cDNA library; anti-oncogene; effector; screening;	
KW KM	transmembrane signalling; activator; inhibitor; modulation;	
KW KM	cellular metabolism; dephosphorylation; prevention; cell growth;	
KW KM	oncogenic transformation; identification; susceptibility; cancer;	
KW KM	diabetes; disease; cellular phosphotyrosine metabolism; ds.	
OS XX	Mus musculus.	
FH XX	Key	Location/Qualifiers
FT XX	CDS	259..2640
FT XX		/*tag= a
PN XX	US5538886-A.	
XX PD	23-JUL-1996.	
XX PF	11-JUL-1990; 90US-0551276.	
XX PR	10-FEB-1993; 93US-0015985.	
XX PR	11-JUL-1990; 90US-0551276.	
XX PA	26-FEB-1991; 91US-0654188.	
XX PA	(UYNV ) UNIV NEW YORK STATE.	
PI XX	Sap JM, Schlessinger J;	
PI XX		
DR XX	WPI: 1996-353827/35.	
DR XX	P-PSDB; AAM02282.	
XX XX	DNA encoding receptor-type protein tyrosine phosphatase - 1s	
XX XX	potential anti-oncogene and effector of trans:membrane signalling	
XX XX	Example 6; Columns 45-48; 50pp; English.	
CC CC	The present sequence encodes murine receptor type tyrosine	
CC CC	phosphatase (RPTP)-alpha, which was isolated from a mouse brain	
CC CC	cDNA library screened with a probe encoding the intracellular and	
CC CC	transmembrane domains of human p200 glycoprotein. RPTP are	
CC CC	potential anti-oncogenes and effectors in transmembrane signalling.	
CC CC	They can be used to screen for cDps, which are specific activators	
CC CC	or inhibitors, for modulating cellular metabolism. Cdds that	
CC CC	activate RPTP cause dephosphorylation and so might prevent cell	
CC CC	growth and oncogenic transformation, while over activity of RPTP	
CC CC	may be involved in diabetes susceptibility. Detection of normal or	

123 A; 123 C; 124 G; 642 T; 0 other;

OV 195 caottocct...  
v, mismatches 650; Indels 15; Gaps 2;

Db	1891	aaccticcagccaacatgaaagaaacccggtttacagatcatccacatagaaatttaac	1950
Qy	1143	cgtgtgtgtctgcagcccatccgtgtgtgtgtgtgtgtgtgtgtgtactaatcatgtcagtgctc	1202
Db	1951	agatgtatcatctccagccaacacgagtcggaagaaacacagatactgttagacgcatcttc	2010
Qy	1203	ctgtatgttttatagacagcagaagagccctacataagctatcacagggccctctgcagagagc	1262
Db	2011	atgtatgtatgaaccggaagaagaactcctcatctgtccagccagggccctctctccacacg	2070
Qy	1263	accgagagactctctgcgcatactgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1322
Db	2071	atgtagaagactctctgcggaatgtctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2130
Qy	1323	aagcttcgggagaatgtgcagggagaagaatgtccacacagtactgtgtccacagagagcgcttcgct	1382
Db	2131	gaactcgtgaagagaagagccaggaagaaagtgtgtccagtaactgtgtgtgtgtgtgtgtgtgt	2190
Qy	1383	cgctacccaagtaactgt	2190
Db	2191	tccttcaggagacatcacaggttgtagctgtgaabaaagagagagaaatgtgaaagctacactgtc	2250
Qy	1443	ctgtagttccaaggtcagcagatgtgcgcggatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2250
Db	2251	cgagagctctctgtgtccacccaacacccaggagaaacagatgtcgtgcgaatctccggacgttccc	2310
Qy	1503	ttcacagaactgtgcagagcagcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2310
Db	2311	ttccacagctgtgcgt	2370
Qy	1563	gggcaggtgtcataagaacccaagtgcaagctttgtgacagagatgtgtgtgtgtgtgtgtgtgtgt	2370
Db	2371	gcacagcagttgcagaagaacgacgcagcagcagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2427
Qy	1623	agtgctgt	2427
Db	2428	agtgctgt	2487
Qy	1683	cgctatgaaggt	2487
Db	2488	aaagcagaagagaattttatgaatgtcttccaaactgttcaagaagcctgtgcgcgcagtgagcca	2547
Qy	1743	gccacgtgtgcagacagagagacacatlatcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2607
Db	2548	caacatgtgtcagacacactgtgaacacagtatgaattctgtccacaaggtgtgtgtgtgtgtgtgtgt	2607
Qy	1803	ggcagcttgcacacactatgcaa 1824	
Db	2608	gacgcctttcaagttatgtgca 2629	

Search completed: August 21, 2001, 20:30:20  
Job time: 7623 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2001, 18:17:52 ; Search time 2512.41 Seconds

(without alignments)  
13044.465 Million cell updates/sec

Title: US-09-719-272-1  
Perfect score: 3467  
Sequence: 1 gatcgcgacgaaggaatcc.....attgaataacagatttct 3467

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.





RESULT	2
AL575903/C	
LOCUS	AL575903
DEFINITION	AL575903 865 bp mRNA
ACCESSION	AL575903 LTI_NFL006.Plz Homo sapiens CDNA clone CS0DI067YH1.1
VERSION	AL575903
KEYWORDS	AL575903.1 GI:12937524 EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	TITLE
1 (bases 1 to 865)	Ll.W.B., Gruber,C., Jesse,J., and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope
2 (bases 1 to 865)	Catarrhini; Homnidae; Homo.
3 (bases 1 to 865)	Eutheria; Primates; Catarrhini; Homnidae; Homo.

**FEATURES**  
source  
1.865

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1067YH11"
/clone_lib="LTI_MFL006_PL2"
/tissue_type="placenta"
/node=Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filang@lifetech.com url :
http://fulllength.invitrogen.com"
205 a 230 c 205 g 220 t 5 others

```

Query Match	23.4%	Score 809.8;	DB 106;	length 865;
Best Local Similarity	97.8%;	Pred. No. 7.2e-176;		
Matches 850; Conservative	2;	Mismatches 11		

Oy	2553	ccagtcgtgctttaaattacaagcccgaaccacacaga	tgtcttggaagcctggcaaa	2612
Db	865	CCCAAGGGGGTTACATTCACAGGCCAAGAACCACAG	CAGTGTGTTGGGAAGCTCGCAA	806
Oy	2613	gcactccatacatcgcttgccaagggttaaacaaaacaa	aanaaccaaanaa	2672
Db	805	GGCATTCTCATCACCATGTGTTGCCAAAGTTAAAA	CAAAAACAAAAAACCAANANA	746

[illegible]

FEATURE	VALUE
LOCUS	AUI23737
DEFINITION	AUI23737 833 bp mRNA
ACCESSION	AUI23737 NT2RM2 Homo sapiens cDNA clone n72RM2000936 5', mRNA
VERSION	AUI23737
KEYWORDS	AUI23737.1 GI:10948453
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE	1 (bases 1 to 833)
JOURNAL	Ota, T., Wakamatsu, A., Oawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
	Isozaki, T.
	Human cDNA project (Ota, T., Wakamatsu, A., Oawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S., Isozaki, T.)
	Unpublished (2000)

## COMMENT

Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3951  
Fax: 81-438-52-3952  
Email: genomics@hri.co.jp  
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix  
Research Institute; cDNA library construction: Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.  
Location/Qualifiers  
1. 833

## FEATURES

source

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="NT2RM200936"  
/clone\_1id="NT2RM2"  
/cell\_type="teratocarcinoma"  
/note="Vector: PMEBFL3; mRNA from uninduced NT2 neuronal  
precursor cells"  
BASE COUNT 185 a 242 c 248 g 154 t 4 others  
ORIGIN

Query Match 22.8%; Score 790; DB 107; Length 833;  
Best Local Similarity 98.1%; Pred. No. 2,6e-171;  
Matches 818; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

Oy 1215 agagcagaagcctcatagctacagagagcctctgacagagacacagagactc 1274  
Db 1 AGACAGGAGAGGCTCATATGCTACACAGGGCTCTTGACAGAGACCGAGACTTC 60  
Oy 1275 tggcgctatctatgagacaaattccacatcatctgctatgacaaagctcgagag 1334  
Db 61 TGGCGCATGCTATGCGAGCAAAATTCACCATCATGCTATGCTGACCAAGCTGGGAG 120  
Oy 1335 atggcgagagagaattccacagctactgagcagagagcgtctgctctaccagatc 1394  
Db 121 ATGGCGAGGAGAAATGCCACAGTACTGCGCCAGAGAGCGCTGCTGCTACCAATAC 180  
Oy 1395 ttgttgctgacagatgagctgagtaacaatgcccagctatatactctgagatcaag 1454  
Db 181 TTTGTGTTGACCCGATGCTGAGTACAAATGCCCAATATCTCTGCTGAGTTCAAG 240  
Oy 1455 gtacagatgcccggagatgagcagtaagaacatccgagcttcacagactgag 1514  
Db 241 GTACCGATGCCGGGATGGGAGTCAAGCAAAATCCGGAGTTCACTTCACAGACTGG 300  
Oy 1515 ccaagcagagcgtgcccacagacagcgagagatcattgacttcatctggcaggtcat 1574  
Db 301 CCAGACAGGCGGTGCCCAAGACAGGCGAGATTCATTGACTTCATCGGCGAGGTCAT 360  
Oy 1575 aagaccaaagagcatttggagagagatgagcctatcacagtgctcagtgctgagctg 1634  
Db 361 MAGACCAAGAGACATTTGGAGAGGATGGCTTATCAAGGTGCACTGACAGTGGCGCTG 420  
Oy 1635 ggcgcacacggggtgtcatcactctgagacatgctctgagagcagctatgagagc 1694  
Db 421 GCCCCACCGGGGTCTCATGCTCTAGCATCTCTCTGGAGCGCATGCTTACGAGGGC 480  
Oy 1695 gtggtcgaatgttttcagacccgtgaagacccctgctacacagcgtctctgacag 1754  
Db 481 GTGTCGACATGTTTCAGACCGTAAAGACCTGCTGATACAGAGTCTGCAATGGTGCAG 540  
Oy 1755 acagagagacagatcagctgtgtacagctgagccctgagagtaactctggcagctt 1814  
Db 541 ACAGAGGACCAAGTATCAAGTGTGTACCTGCGCCCTGGAGTACTCGGACGCTTTGAC 600  
Oy 1815 caactatcaagatatacagctctccctctctctcgcacaccccgagcgtgggagctccga 1874  
Db 601 CACTATGCAAGTACTACCGCTCCCTCTCTCTGCGACACCCCGCGTGGGCTTCCGA 660

Oy 1875 ggggaccagctctctgagcctatcacaccatcgtccagccctcctacagagatgctgt 1934  
Db 661 GGGGACCCAGCTTCTGTGACCCATACCGACATCTGTCAG-CTTCTACGAGATGCTGT 719  
Oy 1935 cactgacagagcctacagccacagggagatcacagcgtttcaggaagcttcacacacata 1994  
Db 720 CACTGCGAGAGCCACAG-CCACGGGATTCACAGCGTTTCAGAACTTCCACACCATCA 778  
Oy 1995 gagaagctagaacatccctgggcaagtgatgagccagcagagcagcagctgtg 2048  
Db 779 GAGAGCTTGAACATCTCCCTGGCGAAGTGGATGNCACANGCAGCACTTGGG 832

## RESULT

4  
Bg470062  
LOCUS Bg470062 913 bp mRNA 1 EST 21-MAR-2001  
DEFINITION 602533550P1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:4660956 5',  
RNA sequence.  
ACCESSION Bg470062  
VERSION Bg470062.1 GI:13402337  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: c9abps-f@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMU at:  
http://Image.lim.gov  
Plate: LLCM1459 row: d column: 13  
High quality sequence stop: 758.

## FEATURES

source

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4660956"  
/clone\_1id="NIH\_MGC\_15"  
/tissue\_type="adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: colon; Vector: pOTB7; Site:1; XhoI; Site:2;  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)"  
BASE COUNT 212 a 257 c 269 g 175 t  
ORIGIN

Query Match 21.7%; Score 753; DB 154; Length 913;  
Best Local Similarity 96.3%; Pred. No. 8,8e-163;  
Matches 856; Conservative 0; Mismatches 25; Indels 8; Gaps 8;

Oy 940 acaagaggggctgcccgaacctgtatgcccacatcagaagctggcgagctgc 999  
Db 2 ACAAGAGGCTGCTGCCCGCACTATGACCATTCAGAACTGGCCAAAGTGCCTC 61  
Oy 1000 caggggagagtgtagcagcagatgagcttaagtctgagcagctccaaagcgc 1059  
Db 62 CAGGGAGAGTGTGACCGCCATGTGAGACTCTGAGTTCAAGTCTGCGCAGCTCAAGGCC 121  
Oy 1060 acacgctccgcttcatcagcgcaacctgacctgcaacaagtccaagacggctgtga 1119

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3951  
Fax: 81-438-52-3952  
Email: genomics@hri.co.jp  
HRI human cDNA project, 5'- and 3'-end one pass sequencing: Helix  
Research Institute; cDNA library construction: Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.  
Location/Qualifiers

1. .7777

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1001540"
/clone_lib="HEMBA1"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/note="Vector: pME18SFL3"
216 c 231 g 145 t
4 others

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21.5%;	Score 745.2;	DB 107;	Length 777;
ity 98.8%;	Pred. No. 5.4e-161;		
conservative	0;	Mismatches 7;	Indels 3.
			Coverage 2

Accession	Gene	Length (bp)
U00096	capB	919

TACATGCTGCAGACGAGGACCACTACGTCCTTCATCCATGAGCGCGTCT 60

accgtgcgcgcacacacagaggtgcctgcgccgcbaacctgtatgcgccacatcca 979

CGTGGGCCACACAGAGGTGCTGCCCGCAACCTGTATGCCACATCCA 120

aaagtgcctccagggagagtgtagccgcgcacatgagctcgagttcnaagt 1039

AAAGTGCCCTCAGGGGAGAGTGTGACCGCCATGAGAGCTCGAGTTCAAGTT 180

ccaaagccccaacacgtcccgcttcatacgcgcgaacctgcccctgcacaa 1099

CCAAAGCCCCACACGTCCTCCGCTTCATCAGCGCCCAACCTGCGCCCTGCACAA 240

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Db 602 GCGGAGGCAATTCATTGACTTCAATCGGCGAGGTGCTAAGAC--AAGAGCAATTTGGAGAG 659
Oy 1599 gatggccatccagcagtgctcagcagtgctcggtcggtggcagacc-gggtgttcatcac 1657
Db 660 GATGGCCCTATACGCGTACCTGACGAGTCTGCGCGCGCGCCAGCGGGGGGTTCATCAC 719
Oy 1658 tctgagcatcgtcctcgagcagcagtgctcaggtatgagggcgtgtgacatgttccagacct 1717
Db 720 TCTGAGCATCGTCTCGAGCGCCAGT--GCTATGAAGGCG--GGCGACCATGTTCAAGAACCTG 777
Oy 1718 gaagccctcgtcagcagcagcgtcctgccaatggtgagacagagagacagatcagcgtgtg 1777
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Db 834 C 834

RESULT 9
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LOCUS AUI24217 NT2RM2 Homo sapiens cDNA clone NT2RM2001847 5', mRNA
DEFINITION AUI24217
sequence:
ACCESSION AUI24217
VERSION AUI24217.1 GI:10948933
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 739)
AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
Iisaga,T.
TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
Y., Sugano,S., Iisaga,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Iisaga
Genomics Laboratory
Helix Research Institute
1332-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomicehri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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precursor cells"

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Db 61 cccccggccggagacacatggcagatcttcggaatggtgtggaacagcagcagcagc 120
Oy 440 tgttgatcatgatacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 499
Db 121 TGTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
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Db 181 ACCCGGTGACACCGAGACTGTGCGCTTATTCAGGTGACCTGTTGACACAGTGAAGCT 240
Oy 560 ggcacacacacacacacacacacacacacacacacacacacacacacacacacacac 619
Db 241 GGCACATACACTGTGCGCTTGTGCACTTCACACACAGTGTGCTCCAGTGAAGGCTGA 300
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Oy 1039 tcttgccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1056
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RESULT 10
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LOCUS BF205938
DEFINITION BF205938 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4098064 5',
mRNA sequence.
ACCESSION BF205938
VERSION BF205938.1 GI:11099624
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE 1 (bases 1 to 809)  
 NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: c9apbs-f@mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: LLCM966 row: f, column: 17  
 High quality sequence stop: 683.

## FEATURES

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 /note="Organ: brain; Vector: pOPB7; Site: 1: XhoI, Site: 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library." 154 t  
 BASE COUNT 180 a 230 c 245 g  
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 Db 3 ATGAGGGGCTGTGAGGCTGCGCCAGCTGGCCACACAGTGGCTGCCCAACCTGT 62  
 Oy 967 atgccacatccagaagctggggagtgctcccaaggagagtgtagccgcatgagc 1026  
 Db 63 ATGCCACATCCAGAAAGCTGGGCGCAAGTCCCTCCAGGGAGAGTGTGACCCCATGAGC 122  
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 Db 123 TCGAGTTCAAGTTGCTGGCGACCTCCAAAGCCACACGTCCTCCCTCATCAGCCCAAC 182  
 Oy 1087 tggcctgcaacaagttcaagaacggcgtggtgaacatcagcctacgaattgacccgtg 1146  
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 Oy 1147 tgtgtcgcagcccaatccgtgtgtgtgagggctgtgactacatcaatgccaagcttctg 1206  
 Db 243 TGTGCTCTCACCCATCCGTGTGTGAGGGCTGTGACTACATCAATCAAGCCACCTCTCG 302  
 Oy 1207 atggtatagacagagaagccttaactagctacacaggggctctgagagagagacag 1266  
 Db 303 ATGTTATAGACAGAGAGGCTCTACTACTACAGAGGGGCTCTGGGAGAGAGACAGC 362  
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 Oy 1686 tatgagggcgtgtgtc 1700  
 Db 781 AAAGCGGGGCTGCAC 795

RESULT 11  
 LOCUS A0118895 732 bp mRNA  
 DEFINITION A0118895 HEMBA1 Homo sapiens CDNA clone HEMBA1004591 5', mRNA  
 ACCESSION A0118895  
 VERSION A0118895.1 GI:10934130  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Salto.K., Kawai.Y.,  
 Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and  
 Isogai.T.  
 HRI human CDNA project  
 Unpublished (2000)  
 CONTACT: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3951  
 Fax: 81-438-52-3952  
 Email: genom@shri.co.jp  
 HRI human CDNA project; 5'-63'-end one pass sequencing; Helix  
 Research Institute; CDNA library construction; Department of  
 Virology, Institute of Medical Science, University of Tokyo, and  
 Helix Research Institute.

FEATURES  
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 Db 1 CTATTCAGGTGACCTGTTGGACACAGTGGAGCTGGCCACATACATGCTGCGACCTTC 60  
 Oy 585 gcactccacaagatggtccagtgagagcgtgagcgtgcagttcagttcagttcagtcg 644



DEFINITION	602363412p1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4471731 5', mRNA sequence.
ACCESSION	BC251541
VERSION	BC251541.1 GI:12761357
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 934)
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabs-remail@hhi.gov">cgabs-remail@hhi.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LHAM10291 row: h column: 04 High quality sequence stop: 794. Location/Qualifiers 1: 934 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4471731" /clone_1lb="NIH_MGC_90" /isuse_type="adenocarcinoma, cell line" /note="Organ: liver, Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."
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Db 61	tgctgttaccgcgaatgctgtgagtaacaatgcccagatcatctcgtgcgtgagttcaagt 120
Oy 1457	caaggatgccgggagatgaggcaagtaacaaatccggcaggttcagattcacagactgagc 1516
Db 121	cacgcgatgccgggagatgaggcaagtaacaaatccggcaggttcagattcacagactgagc 180
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Db 181	agaagcagggcgtgtcccaagacagcggaaggaattcatcttaactcatccggcagaagtcatra 240
Oy 1577	gaccagaagcagattgttgacaggaacgaggcctatcaacgtygtcaccttcagtgccggcgttgg 1636
Db 241	gaccagaagcagattgttgacaggaacgaggcctatcaacgtygtcaccttcagtgccggcgttgg 300
Oy 1637	ccgcacccggggtgtgtcatcaactctgagcatcgctctgtgagcagatgagctatgagggcgt 1696
Db 301	ccgcacccggggtgtgtcatcaactctgagcatcgctctgtgagcagatgagctatgagggcgt 360
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RESULT	1	ALIGNMENTS
DEFINITION	HSIAR	
LOCUS	Human mRNA for LCA-homolog. LAR protein (leukocyte antigen related).	
ACCESSION	7702 bp	PRI
VERSION	Y00815	19-SEP-1995
KEYWORDS	Y00815.1 GI:34266 antigen; cell surface glycoprotein; glycoprotein; immunoglobulin superfamily; LAR gene; leukocyte common antigen; neural cell adhesion molecule; transmembrane protein.	
SOURCE	Homo sapiens	
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE	1 (bases 1 to 7702)	
AUTHORS	Salto, H.	
TITLE	Direct Submission	
JOURNAL	Submitted (15-SEP-1986)	
REFERENCE	Biney Street, Boston, MA 02115	
AUTHORS	2 (bases 1 to 7702)	
TITLE	Steuil, M.-T. Krueger, N.X., Hall, L.R., Schlossman, S.F. and Salto, H.	
JOURNAL	A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen	
REFERENCE	J. Exp. Med. 168 (5), 1523-1530 (1988)	
AUTHORS	3 (bases 1 to 7702)	
JOURNAL	Schepens, J.T., van den Maagdenberg, A.M., Schepens, J.T.,	
REFERENCE	Mechnis, D.O., Geurts van Kessel, A., Miering, B. and Hendriks, W.J.	
AUTHORS	The mouse gene Pcp1f encoding the leukocyte common antigen-related molecule LAR: cloning, characterization, and chromosomal localization	

JOURNAL MEDLINE 95394448

Genomics 27 (1), 124-130 (1995)

FEATURES

Source

Location/Qualifiers

1. 7702

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/note="put. extracellular domain"

4121. 4192

/note="put. transmembrane domain"

4193. 6061

/note="put. cytoplasmic domain"

BASE COUNT 1636 a 2286 c 2292 g 1488 t

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Query Match 99.98; Score 3463; DB 93; Length 7702;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3463; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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0y 65 ctaccagaccacccagatctcgagaccacccacccatcccatcccgacttgcgagaca 124

Db 4300 CTACGACGCCACCGATGTCGAGACACCCACCCATCCCATCAGCAGACTGGCGGACAA 4359

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Oy	725	cgaagaaggccaaatgttgttgaatccttgcagcggcggtgtgggcgcacacggcttcatcgt	784
Db	4960	CGCAGGGCCCAATGGTGTGTGCACATGCAAGGGGGCGTGGGCCGACACGGCTCTTCAATCGT	5019
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OY	1265	cgaagactctcggcgacagctcgtatggagagacacatccacatcgtcatgtcagccaa	1324
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OY	1325	gcttcggagagatgggacagaggagaaatgcacacagtaactggccacagagagcctcgtcgg	1388
Db	5560	GCTTCGGGAGATGGGACGAGGAGAAATGCCACACAGTACTGGCCGACAGACGCGCTCTGCG	5619
OY	1385	ctaccagtaacttgcttgcttgaccggaatggcctggatcaacaatgcgccaglatatccctgg	1444
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OY	2045	gtggccctctcgttccacacagaccacacacccctggagccgctctcaagctctgtgtgcctcc	2104
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Db	7660	TGCATATTTCTTGATGGTAATTAATTGAATAATACAGATTCT	7702

  

RESULT	2
LOCUS	M60103 4190 bp mRNA
DEFINITION	Rattus norvegicus leukocyte common antigen related protein mRNA, 3'
ACCESSION	M60103
VERSION	M60103.1 GI:205130
KEYWORDS	leukocyte common antigen related protein.
SOURCE	Rattus norvegicus adult hypothalamus, CDNA to mRNA.
ORGANISM	Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (sites)
TITLE	Struill, M., Krueger, N.X., Hall, L.R., Schlossman, S.F. and Salto, H. A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen
JOURNAL	J Exp. Med. 168, 1523-1530 (1988)
REFERENCE	2 (bases 1 to 4190)
AUTHORS	Pol, D.A., Woodford, T.A., Remboutske, E., Haun, R.S. and Dixon, J.E. Cloning, bacterial expression, purification and characterization of the cytoplasmic domain of rat LAR, a receptor-like protein tyrosine phosphatase
JOURNAL	J Biol. Chem. 266, 19688-19696 (1991)
FEATURES	92011772
Source	Location/Qualifiers
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BASE COUNT	942 a	1167 c	1351 g	930 t
ORIGIN				

  

Query Match	Best Local Similarity	84.2%	Score 2335.6	DB 94	Length 4190
Matches 2927	Conservative	0	Mismatches 474	Indels 77	Gaps 23

  

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Db	771	CGGCTGAAGAGCTCCCTGTTGGCCCACTCTTCTACCTGTGGAAATGCAAGGCTTAA	830

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17	1277.4	36.8	5383	95	RATLARPTP	X82288 M. muscu
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20	1273.2	36.7	5690	9	AR060681	L19933 Rattus norv
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22	1256.2	36.2	6363	97	HS053234	U35234 Human prote
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24	1234.2	35.3	6412	95	RATPTP1	L19180 Rat recepto
25	1218.4	35.1	7297	8	AF197945	L19180 Rat recepto
26	1170.6	33.8	4613	8	CHKCRYP	L3780 Gallus gall
27	1095.8	31.6	6263	97	HUMPTPD	L3829 Homo sapien
28	1094.6	31.6	4584	93	HSPTPD	X54133 Human Hprt
29	1074.8	30.6	4584	93	HSPTPD	AF198450 Xenopus 1
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31	1059	30.5	4555	45	E09890	E09890 Mouse CDNA
32	1017.6	29.4	4555	94	MUSMPTPA	D13803 Mouse mRNA
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36	919	26.5	1489	8	AB033581	AB033586 Branchios
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38	868.4	25.0	1851	8	AB033586	AB033586 Branchios
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41	830.8	24.0	1194	95	RNU03273	U03273 Rattus norv
42	818.4	23.6	4314	5	AF017084	AF017084 Hirudo me
43	796	23.0	6227	5	AF017083	AF017083 Hirudo me
44	765.6	22.1	6490	6	DMDLAR9	U36857 Drosophila

## ALIGNMENTS

RESULT	1	ALIGNMENTS
LOCUS	7702 bp mRNA	19-SEP-1995
DEFINITION	Human mRNA for LCA-homolog. LAR protein (leukocyte antigen related).	
ACCESSION	Y00815.1	GI:34266
VERSION	Y00815.1	GI:34266
KEYWORDS	antigen; cell surface glycoprotein; glycoprotein; immunoglobulin superfamily; LAR gene; leukocyte common antigen; neural cell adhesion molecule; transmembrane protein.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	Saito, H.	
TITLE	Direct Submission	
JOURNAL	Submitted (15-SEP-1989) Saito H., Dana-Farber Cancer Institute, 44	
REFERENCE	Binney Street, Boston, MA 02115	
AUTHORS	Streuli, M., Krueger, N.X., Hall, L.R., Schlossman, S.F. and Saito, H.	
TITLE	2 (bases 1 to 7702)	
JOURNAL	A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen	
REFERENCE	J Exp. Med. 168 (5), 1533-1530 (1988)	
AUTHORS	Schaepeveld, R.O., van den Maagdenberg, A.M., Schepens, J.T., Meghuijs, D.O., Geurts van Kessel, A., Kiering, B. and Hendriks, W.J.	
TITLE	The mouse gene P19f encoding the leukocyte common antigen-related molecule LAR: cloning, characterization, and chromosomal localization	

JOURNAL	Genomics 27 (1), 124-130 (1995)
MEDLINE	95394448
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DB	65 CTACCGAGCCGAGTATGAGAGACCAACCCATCCATCCAGGACTGCGGACAA 4359
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RESULT	2
LOCUS	M60103
DEFINITION	Rattus norvegicus leukocyte common antigen related protein mRNA, 3
ACCESSION	M60103
VERSION	M60103.1
KEYWORDS	leukocyte common antigen related protein.
SOURCE	Rattus norvegicus adult hypothalamus, cDNA to mRNA.
ORGANISM	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (sites)
AUTHORS	Streuli,M., Krueger,N.X., Hall,L.R., Schlossman,S.F. and Salto,H.
TITLE	A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen
JOURNAL	J. Exp. Med. 168, 1523-1530 (1988)
MEDLINE	85035978
REFERENCE	2 (bases 1 to 4190)
AUTHORS	Pot,D.A., Woodford,T.A., Remboutsika,E., Haun,R.S. and Dixon,J.E.
TITLE	Cloning, bacterial expression, purification and characterization of the cytoplasmic domain of rat LAR, a receptor-like protein tyrosine phosphatase
JOURNAL	J. Biol. Chem. 266, 19668-19696 (1991)
MEDLINE	92011772
FEATURES	<p>location=Qualifiers</p> <p>..4190</p> <p>/organism="Rattus norvegicus"</p> <p>/db_xref="taxon:10116"</p> <p>/det_stage="adult"</p> <p>/tissue_type="hypothalamus"</p> <p>&lt;1..2595</p> <p>/codon_start=1</p> <p>/evidence=experimental</p> <p>/product="leukocyte common antigen related protein"</p> <p>/protein_id="AA041510.1"</p> <p>/db_xref="GI:205131"</p> <p>/translation="EKILYNGGSEYVDGHSMRNLADLPNTYSFVLNRRSSAGL  OHVLSIRAPDLPLPKPLPSAFTEDEGRSLSPVOQDSLRFVFIYVPIIDRYGN  LLAPRSTPEELDELELEAIEQEEKORRRROARSLPYAAOVDELPEFTIGDL  KNIGKFTNRPLSDLSYOCFLAELKEPMHKKVASSPDELYVDPAAQDEPRL  LWVGPLVALYLILVIALILFKRRKTRKANGKLFSCQESIDPGQFVENSVEVRL  KYVQGRHDHPIDPIEDLADINERLKANGKLFSCQESIDPGQFVENSVEVRL  KNRYANIAVDHRSVLTISIDVGSQDYNANVLDKRNQNVIAVQGLEPTMDGF  MMEQOATATVVMVTLLEKSRPKCQVYPAGETVEGLIOTVLDVDELATYMTRF  ALHSGSEKRELROFQAMRPHGVEPPIPLFLNRVKAACNLDGPNVHCASG  VGRGCGIVTDALNLEKNEKTVYDIQHTCMKRSQNVNVOEDQYVIFHALLAKM  CGHEVLARLNLAIHOKLQVDPGSESVTAMLEFYLANSKASRFSIALPKNK  NRLLNPELTELTVCLQIRVEGSDYINASFQYROOKAVIATQGLASTEDPR  MLEHNSNTIIVMLTKLREGRKCHQYMPAERSARVQVDPMAEYIMPOYILRER  VTIARQDSRTIRQFQTPMPKGVKPGKEGIDPISGVNHTKDFQGDGPTIVHCA  GVRTQVFVITLIVLERMVEGVDMFQTVLTLTRQNPAMVOTEDYQLCYRALEVL  GSDPHAT"</p>
CDS	

BASE COUNT	942 a	1167 c	1151 g	930 t
ORIGIN				

Query Match	67.4%	Score 2335.6	DB 84	Length 4190
Best Local Similarity	84.2%	Pred. No. 0		
Matches 2927	Conservative	0	Mismatches 474	Indels 77
Gaps	23			

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||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 771 CGGGCTGAAGAGATCTCCCTTTGGCCACACTCTTGTGACCCCTGTGGAAGTTCGGAAGCTTAA 870

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2001, 18:19:42 ; Search time 4532.97 Seconds  
(without alignments)  
11830.364 Million cell updates/sec

Title: US-09-719-272-1

Perfect score: 3467

Sequence: 1 gatacggactgaagactcc.....attgataatcagattct 3467

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
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93: gb\_pi9:\*  
94: gb\_pi10:\*  
95: gb\_pi11:\*  
96: gb\_pi12:\*  
97: gb\_pi13:\*  
98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3463	99.9	7702	93	HSLARR
2	2335.6	67.4	4190	94	M60103
3	1917.2	55.3	6545	95	BATLARA
4	1876.8	54.1	4685	95	BATLARA
5	1694.6	48.9	2202	94	RNLAR1
6	1668.2	48.1	3941	95	RNLAR2
7	1657.8	47.8	152891	62	AC011772
8	1656.8	47.8	128327	79	AL158083

AL158083

9	1588.6	45.8	5723	94	AF300943	Mus muscu
10	1546.6	44.6	2213	95	U00477	000477 Rattus norv
11	1505	43.4	1638	54	G06614	G06614 human STS M
12	1285	37.1	4773	97	HS041725	U41725 Human prote
13	1285	37.1	6000	9	AK031690	AK031690 Sequence
14	1285	37.1	6000	10	161404	161404 Sequence 6
15	1285	37.1	6000	97	HS040317	U40317 Human prote
16	1281	36.9	5978	94	MMPTPNJ3	X82288 M.musculus
17	1277.4	36.8	5383	95	RATLARPTB	L12329 Rat leukocy
18	1277.4	36.8	6469	95	RATLARPTB	L11587 Rat leukocy
19	1276.4	36.8	4724	95	RATLARPTB	L19933 Rattus norv
20	1273.2	36.7	5690	9	AR060681	AR060681 Sequence
21	1273.2	36.7	5690	9	AR064169	AR064169 Sequence
22	1256.2	36.2	6363	97	HS035234	U35234 Human prote
23	1256.2	36.2	6734	94	MSPTPT9	D28530 Mouse mRNA
24	1224.2	35.3	5412	95	RATPTP1	L19180 Rat recepto
25	1218.4	35.1	7297	8	AF197945	AF197945 Xenopus 1
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27	1095.8	31.6	6263	97	HUMPTPD	L38929 Homo sapien
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## ALIGNMENTS

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ACCESSION Y00815.1 GI:34266  
VERSION  
KEYWORDS antigen; cell surface glycoprotein; glycoprotein; immunoglobulin superfamily; LAR gene; leukocyte common antigen; neural cell adhesion molecule; transmembrane protein.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 7702)  
Saito, H.  
TITLE Direct Submission  
JOURNAL Submitted (15-SEP-1988) Saito, H., Dana-Farber Cancer Institute, 44  
AUTHORS Blinney Street, Boston, MA 02115  
2 (bases 1 to 7702)  
REFERENCE 2  
AUTHORS Struill, M., Krueger, N.X., Hall, L.R., Schlossman, S.F., and Saito, H.  
TITLE A new member of the immunoglobulin superfamily that has a  
JOURNAL cytoplasmic region homologous to the leukocyte common antigen  
MEDLINE J. Exp. Med. 168 (5), 1523-1530 (1988)  
AUTHORS 89035978  
3 (bases 1 to 7702)  
REFERENCE 3  
AUTHORS Schapvel, R.O., van den Maagdenberg, A.M., Schepens, J.T.,  
TITLE Weghuis, D.O., Geurts van Kessel, A., Wieringa, B., and Hendriks, W.J.  
Molecule gene Pp1 encoding the leukocyte common antigen-related  
localization

JOURNAL Genomics 27 (1), 124-130 (1995)  
MEDLINE 95394448  
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Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 3463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4300 CTACCAGACCCAGGATGCGAGACCCACCCATCCCATCCGACCTGGGAGCA 4359



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RESULT	2
LOCUS	M60103 4190 bp mRNA
DEFINITION	Rattus norvegicus leukocyte common antigen related protein mRNA, 3
ACCESSION	M60103
VERSION	M60103.1
KEYWORDS	leukocyte common antigen related protein.
SOURCE	Rattus norvegicus adult hypothalamus, CDNA to mRNA.
ORGANISM	Rattus norvegicus
REFERENCE	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
AUTHORS	Rattus.
TITLE	1 (sites)
JOURNAL	Streni, M., Krueger, N.X., Hall, L.R., Schlossman, S.F. and Salto, H.
MEDLINE	A new member of the immunoglobulin superfamily that has a
AUTHORS	cytoplasmic region homologous to the leukocyte common antigen
TITLE	J. Exp. Med. 168, 1523-1530 (1988)
REFERENCE	2 (bases 1 to 4190)
AUTHORS	Poc, D.A., Woodford, T.A., Remboutsika, E., Haun, R.S. and Dixon, J.E.
TITLE	Cloning, bacterial expression, purification, and characterization of
JOURNAL	the cytoplasmic domain of rat LAR, a receptor-like protein tyrosine
MEDLINE	phosphatase
AUTHORS	J. Biol. Chem. 266, 19688-19696 (1991)
TITLE	92011772

  

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Gaps	23			

  

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Query Match 54.1%; Score 1876.8; DB 95; Length 4685;  
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 Matches 2275; Conservative 0; Mismatches 347; Indels 70; Gaps 12;

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Db 1925 GAGCCATACCGACATCTCTCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1984
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REFERENCE 1 (bases 1 to 152891)

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# AUTHORS TITLE JOURNAL REFERENCE AUTHORS

Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 Homo sapiens chromosome 15, clone RP11-134C3  
 Unpublished  
 2 (bases 1 to 152891)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
 Baldwin, J., Barna, N., Beckert, R., Boguslavsky, L., Boukhalter, B.,  
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collamore, A.,  
 Cooke, P., Deatellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,  
 Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Horton, L.,  
 Howland, J., Jodhva, S., Grant, G., Haggos, B., Heaford, A., Horton, L.,  
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 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Tesfaye, S., Turrell, A., Vassiliou, H., Vo, A., Wheeler, J., Wu, X.,  
 Wyman, D., Ye, M., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (14-OCT-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Feb 28, 2000 this sequence version replaced gi:630598.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

## TITLE JOURNAL

Center: Whitehead Institute/ MIT Center for Genome Research  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 Project Information  
 Center project name: 134.C.3  
 Center clone name: 134.C.3

Summary Statistics  
 Sequencing vector: M13, M7815: 100% of reads  
 Chemistry: Dye-terminator Big Dye: 100% of reads  
 Assembly program: Phrap: version 0.960731  
 Consensus quality: 128435 bases at least 400  
 Consensus quality: 143118 bases at least 400  
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 Insert size: 151291; sum-of-contigs  
 Quality coverage: 4.2 in 920 bases; agarose-fp  
 Quality coverage: 4.4 in 920 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently  
 consists of 17 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

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 727 826: gap of 100 bp  
 827 2241: contig of 1415 bp in length  
 2242 2341: gap of 100 bp  
 2342 3786: contig of 1445 bp in length  
 3787 3886: gap of 100 bp  
 3887 7375: contig of 3489 bp in length  
 7376 7475: gap of 100 bp  
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45724 GTGTGCCCCAGGTGATATAGCACACAGGTTAGGCTGTGTGCCACACCCCATGCACCTCAGGGC 45665

```

Quality coverage: 4.76x in Q20 bases; sum-of-contigs quality
coverage: 4.26x in Q20 bases; agarose-ftp
*** NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1
* 14174: contig of 14174 bp in length
* 14175 14274: gap of 100 bp
* 14275 47743: contig of 33463 bp in length
* 47744 47843: gap of 100 bp
* 47844 52973: contig of 5130 bp in length
* 52974 53073: gap of 100 bp
* 53074 61591: contig of 8518 bp in length
* 61592 61691: gap of 100 bp
* 61692 65293: contig of 3602 bp in length
* 65294 65393: gap of 100 bp
* 65394 68160: contig of 2767 bp in length
* 68161 68260: gap of 100 bp
* 68261 72937: contig of 4677 bp in length
* 72938 73037: gap of 100 bp
* 73038 83688: contig of 10651 bp in length
* 83689 83788: gap of 100 bp
* 83789 90410: contig of 6622 bp in length
* 90411 90510: gap of 100 bp
* 90511 128327: contig of 37817 bp in length.
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Best Local Similarity 98.4%; Pred. No. 0;
Matches 1703; Conservative 0; Mismatches 3; Indels 25; Gaps 2
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Db 20154 AGGACAGATACGCTCTACCTACCTGCGCCCTCGAGATACCTCGCAGCTTGACACT 2009*
OY 1819 atgcacgaactacacgcctccctctcctcgccacccccccgctggggtccggaagg 3*

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 Best Local Similarity 90.8% Pred. No. 0;  
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QY 445 tcataatgacacagctcgtgagagaagctccgggtgaaatgtatcagtcctggcaagcc 50.  
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 QY 505 gtgcacacgaagaccgtgacctatcgaatgaacctgttgcacacagtgtgagctgtgca 56.  
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QY	745	actgcagacgcggcggtgtggcgccagccgggtgtgttcattcatgattgatgatgtgtgttgagac	804
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QY	805	ggatgaagacacgaagaacggttgcacatcatatggccagtgtaactgtatgatgtcaacaga	864

[illegible]

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1465 ccggagatgggcagtcgaagagcaatccggcaggtccagctccagatcagcagccagaagcagg 1524  
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Db 2131 AGACGTGTCYGGGGAGACCTGGCCAGGCGCTTCTCCTGCATCGTGTTCAGAGTT 2190  
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RESULT 11  
G06614  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Human STS WI-7601. DNA STS 19-OCT-1995  
G06614  
G06614.1 GI:859859  
STS sequence: primer, sequence tagged site.  
human STSs derived from sequences in dbEST and the Unigene  
collection.  
Homo sapiens  
Eukaryota; Eukaryota; Eukaryota; Metazoa; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 1638)  
Hudson, T.  
Whitehead Institute/MIT Center for Genome Research, Physically  
Mapped STS  
Unpublished (1995)

JOURNAL  
COMMENT

Contact: Thomas Hudson  
Whitehead Institute/MIT Center for Genome Research  
Whitehead Institute for Biomedical Research  
9 Cambridge Center, Cambridge MA 02142 USA  
Tel: 617 252 1800  
Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu

Primer A: CAGACGACATCTGTTTCAGC  
Primer B: GTTTCAGCAGACCAAGC  
STS size: 333  
PCR Profile:  
Presoak:  
Denaturation:  
Annealing: 56 degrees C  
Polymerization:  
PCR Cycles: 35  
Thermal Cycler:  
Protocol:  
Template: 10 ng  
Primer: each 5 pM  
dNTPs: each 4 mM  
Tag Polymerase: 0.025 units/ul  
Total Vol: 20 ul

Buffer:  
MgCl2: 1.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 9.3

FEATURES  
source  
STS  
primer\_bind  
BASE COUNT  
ORIGIN

Prepared with primer pairs derived from Y00815 -- Unigene.  
Location/Qualifiers  
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Query Match 43.4% Score 1505; DB 54; Length 1638;  
Best local Similarity 91.9%; Pred. No. 0;  
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 OY 1890 ctgagccataccgacatcgtccagccctctcagcagatctgtcactgtgcagagca 1949  
 DB 61 ctgagccataccgacatcgtccagccctctcagcagatctgtcactgtgcagagca 120  
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 DB 181 cccctggagcagtgagtgagcccgagagagcagctgtgcccctctgtccacagagcca 240  
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 DB 421 ggggtgggttacttctgttcttcttcttcttcttcttcttcttcttcttcttcttct 480  
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 Endo, N., Rutledge, S.J., Opas, E.E., Vogel, R., Rodan, G.A. and  
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 Human protein tyrosine phosphatase-sigma: Alternative splicing and  
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 J. Bone Miner. Res. (1995) In press  
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 Endo, N., Rutledge, S.J., Opas, E.E., Vogel, R., Rodan, G.A. and  
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 Direct Submission  
 Submitted (30-NOV-1995) Jeff Aaronson, Bioinformatics, Merck & Co.,  
 Inc., PO Box 2000, MS R80A-1, 126 E. Lincoln Ave., Rahway, NJ  
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Db 4978 CTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5037
Oy 1109 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1168
Db 5038 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5097
Oy 1169 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1228
Db 5098 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5157
Oy 1229 CCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1288
Db 5158 CCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5217
Oy 1289 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1348

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Db 5218 GGAGAACATTCGACGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 5277
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Oy 1409 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1468
Db 5338 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5397
Oy 1469 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1528
Db 5398 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5457
Oy 1529 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1588
Db 5458 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5517
Oy 1589 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1648
Db 5518 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5577
Oy 1649 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1708
Db 5578 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5637
Oy 1709 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1768
Db 5638 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5697
Oy 1769 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1828
Db 5698 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5757
Oy 1829 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1857
Db 5758 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5786

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Search completed: August 21, 2001, 20:34:57  
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